

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 11, 2002, 11:42:09 ; Search time 6528.21 Seconds  
(without alignments)  
6407.126 Million cell updates/sec

Title: US-09-864-680-2  
Perfect score: 3099  
Sequence: 1 caaatacttccttgagtgaa.....tttagtttaaaaaaaaaa 3099

Scoring table: IDENTITY\_NDC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 segs, 6748477542 residues  
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: em\_estba:\*  
2: em\_estbhm:\*  
3: em\_estcin:\*  
4: em\_estlmu:\*  
5: em\_estlov:\*  
6: em\_estlpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_estl1:\*  
10: gb\_estl2:\*  
11: gb\_hlc:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	145.2	4.7	663	10	BI433950 EST536711
2	135.4	4.4	535	10	BM109555 EST557091
3	135.4	4.4	691	10	BI406780 180E06 Ma
4	135.2	4.4	635	9	AW979731 EST341354
5	126.2	4.1	669	10	BM411546 EST585873
6	125.4	4.0	607	10	BI943480 EST544695
7	122.2	3.9	659	10	BE923412 EST427181
8	120.4	3.9	426	10	BM408141 EST582468
9	119.6	3.8	515	10	BI934083 EST53972
10	118	3.8	639	12	BI42383 TDGDO21TH
11	113	3.6	617	10	BE460726 EST412145
12	113	3.5	417	9	AM030063 EST273318
13	108.4	3.5	417	9	AM030063 EST273318
14	107.2	3.5	417	9	AM030063 EST273318
15	105.4	3.4	660	9	AM216532 EST295246
16	104.8	3.4	524	12	BI42479 TDGDP27TH
17	103.4	3.3	576	9	AI772710 EST253810

18	102.8	3.3	464	10	BF114223 EST441813
19	100.6	3.2	579	9	AM034628 EST278312
20	100.4	3.2	573	10	BM407382 EST581709
21	100.2	3.2	643	9	AM622905 EST306975
22	98.8	3.2	358	10	BF053416 EST348646
23	98	3.2	558	10	BI425924 EST574408
24	97.2	3.1	593	10	BM110993 EST558529
25	97	3.1	800	10	BI421945 EST532611
26	96.4	3.1	779	10	BG596578 EST495256
27	95.2	3.1	526	9	AM217536 EST296250
28	94.8	3.1	587	9	AM934420 EST360253
29	94.4	3.0	323	9	AM933105 EST358948
30	90.8	2.9	725	10	BI177939 EST518884
31	90	2.9	339	10	BI176878 EST517823
32	89.8	2.9	414	9	AM737247 EST38674
33	88.8	2.9	784	10	BI432945 EST535706
34	83.8	2.7	604	10	BI179578 EST520523
35	81.8	2.6	785	10	BM404923 EST579250
36	81.2	2.6	686	10	BI920482 EST540417
37	81.2	2.6	692	10	BI920471 EST540406
38	81.2	2.6	708	10	BI920408 EST540343
39	80.8	2.6	541	10	BM178803 sa15905
40	80.8	2.6	606	10	BM405792 EST580119
41	79.8	2.6	663	10	BG890386 EST516237
42	79	2.5	471	10	BF054511 EST439741
43	78.8	2.5	555	9	AM737464 EST338807
44	78.6	2.5	433	9	AM031596 EST275050
45	78.4	2.5	396	10	BM409153 EST583480

## ALIGNMENTS

RESULT 1  
BI433950 663 bp mRNA linear EST 21-AUG-2001  
EST536711 P. infestans-challenged leaf Solanum tuberosum CDNA clone  
DEFINITION  
PPC8K40 5' sequence, mRNA sequence.  
ACCESSION  
BI433950  
VERSION  
BI433950.1 GI:15258640  
SOURCE  
EST.  
ORGANISM  
Solanum tuberosum  
potato.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

REFERENCE  
Autors  
Restrepo, S., Griffiths, H.M., Smart, C.D., Cho, J., Chieningo, A.,  
Bougril, O., Buell, C.R., Ronning, C.M., Fry, W.E. and Baker, B.  
Generation of ESTs from potato leaves Challenged with Phytophthora  
infestans, Compatible Interaction  
unpublished (2000)  
JOURNAL  
Contact: Cathy Ronning  
The Institute for Genomic Research  
For clone info: please contact Research Genetics, Libraries  
Division tel 1-800-711-6195, email cdna@resgen.com  
COMMENT  
Seq primer: M13F-R.  
Location/Qualifiers  
1.663  
/organism="Solanum tuberosum"  
/cultivar="Kennedec"  
/db\_xref="taxon:4113"  
/clone="PPC8K40"  
/clone\_1lb="P. infestans-challenged leaf"  
/tissue\_type="leaf"  
/dev\_stage="6 week old"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-). Site\_1: EcoRI; Site\_2:  
XhoI; Whole plants were challenged with 450,000  
sporangia/ml P. infestans US-1(US 940501) in Biotron  
(Madison, Wisconsin). Leaf tissue was collected at 1, 2,  
5, 12, and 24 hours post-challenge and frozen in liquid  
nitrogen immediately upon removal. Kennedec plants showed

FEATURES  
source

no signs of HR. Kathadin plants (susceptible to P. infestans US-1) were used as controls and showed infection. NOTE: We cannot exclude the possibility that this sequence is actually derived from Phytophthora rather than potato.

BASE COUNT 207 a 116 c 137 g 203 t  
ORIGIN

Query Match 4.7%; Score 145.2; DB 10; Length 663;  
Best Local Similarity 54.3%; Pred. No. 1.5e-21;  
Matches 366; Conservative 0; Mismatches 293; Indels 15; Gaps 3;

Qy 666 aaagaagttacaatgaatcaatctatccgttttgatgcttcacgtggtcc 725  
D 2 AGAAAGCTTAATGATCTTATTTGTTCTGATTTGTAATGATGATGGTCA 61  
Qy 726 atattcaacgcacacacacacacacacacacacacacacacacacac 785  
D 62 ATCTCCGAAAAATTCATCAGACAAATGCTTTGAAAGTTGCTATGCAAT 121  
Qy 786 atgataagcaggttaagatgattgtaagcagagcagacatgttacaga 845  
D 122 AGCATCAAGAAATCA-----GCCATGATCACTAATGAGATGATGATG 172  
Qy 846 ttaagaagaagaggtacttaattgtcttgatgatactgagttggaagt 905  
D 173 CTGAAGGCGCAGAGATTTCTAATGTCATGATGATGATGATGATGATG 232  
Qy 906 ggcgtgagcagatgcttccacacacacacacacacacacacacacac 965  
D 233 CAATGCAAGAAATTTTCCAAATGATGACAAATTAACCTAATGATG 292  
Qy 966 cgtatgataagatgactgttgcgtggtgtaagaaatttcttcgtgag 1025  
D 293 CTCAAGATATGTTGCTGATGATGATGATGATGATGATGATGATGAT 352  
Qy 1026 atgataagaatgagatgagatgagatgagatgagatgagatgagat 1085  
D 353 CTAAAGCTAGAAATGATGATGATGATGATGATGATGATGATGATGAT 412  
Qy 1086 ccaatagatgctgagactgttgcgtggtgtaagaaatttcttcgtgag 1145  
D 413 CTTGCTGCTGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 472  
Qy 1146 acattgtcgtggtgagaggtctt---caatctaaagacacacacac 1202  
D 473 TCGGTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 532  
Qy 1203 actgtctaaagatgctgacatgctgacacacacacacacacacac 1262  
D 533 AAGGTTAGAGAAATCTGAACCTCTCTTGTGATGAGGTGTC---CGA 589  
Qy 1263 gtcgttggtgagttacacacacacacacacacacacacacacacac 1322  
D 590 ATTCTTCTCTGAGCTATATTAATTAATTAATTAATTAATTAATTAAT 649  
Qy 1323 ggaattttccaga 1336  
D 650 GGAGGGTTTCAGA 663

RESULT 2  
BM109555 535 bp mRNA linear EST 26-NOV-2001  
LOCUS BM109555  
DEFINITION EST557091 potato roots Solanum tuberosum cDNA clone cPRO4H13 5' end  
ACCESSION BM109555  
VERSION BM109555.1 GI:17070574  
KEYWORDS EST.  
SOURCE potato.  
ORGANISM Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

## REFERENCE

1 (bases 1 to 535)  
van der Hoeven, R., Sun, H., Karameycheva, S.A., Tsai, J., Van Aken, S.,  
Uterback, T., Chiemingo, A., Bougri, O., Buell, C.R., Ronning, C.,  
Tankley, S. and Baker, B.  
Generation of ESTs from potato roots

## JOURNAL

Unpublished (2001)  
Contact: Research Genetics, Libraries Division  
Tel: 1-800-711-6195  
Email: cdna@resgen.com  
For clone info: please contact Research Genetics, Libraries  
Division tel 1-800-711-6195, email cdna@resgen.com  
Seq primer: T3.

## FEATURES

source  
Location/Qualifiers  
1..535

/organism="Solanum tuberosum"  
/cultivar="Kennebec"  
/db\_xref="taxon:4113"  
/clone="cPRO4H13"  
/clone\_1db="potato roots"  
/tissue\_type="roots"  
/dev\_stage="in vitro grown stem cuttings"  
/lab\_host="SOLR"

/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:  
XhoI; supplier: Cornell University, Tanksley lab;  
sequencing: The Institute for Genomic Research. Roots were  
isolated from in vitro grown stem cuttings on CM medium.  
Roots were isolated two weeks after placing the stem  
cuttings from in vitro grown plants on medium."

BASE COUNT 156 a 74 c 134 g 171 t  
ORIGIN

Query Match 4.4%; Score 135.4; DB 10; Length 535;  
Best Local Similarity 57.7%; Pred. No. 2.2e-19;  
Matches 310; Conservative 0; Mismatches 206; Indels 21; Gaps 3;

Qy 862 actaatgcttgatgatatcgtgagttgagtggtgagtgagtgagtgag 921  
D 2 ATTTTATTTGTTGATGATGATGATGATGATGATGATGATGATGATGAT 61  
Qy 922 ttcaactgaagacacacacacacacacacacacacacacacacacac 981  
D 62 TTCCAGATTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 118  
Qy 982 ctgttgatgctggtgagag---aatttcttgcgagtgagcttcaatga 1038  
D 119 GTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 178  
Qy 1039 agattgagctcttcaaaagtgacacatttca-----agtgaagcat 1083  
D 179 AAGTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 238  
Qy 1084 taacataatgagttcagacacacacacacacacacacacacacacac 1143  
D 239 ATATTGATGAATTCGAAAGGTTGAGAAAAAGTTGTAACAAATTCGA 298  
Qy 1144 taactatgctggtggtgagacacacacacacacacacacacacacac 1203  
D 299 TAAATGATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 358  
Qy 1204 ctgttgctaaagatgtaacacacacacacacacacacacacacacac 1263  
D 359 AAGTAGTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 418  
Qy 1264 tgcgttggtgagttcagacacacacacacacacacacacacacacac 1323  
D 419 TTGTTGCTTTGAGCTACAAATCAATCTCTCTCTGGAAGCTCTTTTGC 478  
Qy 1324 gaattttccagaagacagtgatattccagtgagaatttgatgagatcag 1380  
D 479 GAGTTTCCCAAGGCCATGATTTTCTGTGAAGAAATTAATTAATTAAT 535



OY	784	aaatgatgacaggggttaagatgatctggtgaagcagagctagcacacatggtacacgaaaaa	843
Db	266	-----GCTTCCACAGGACCAAGGGGTATGAGAGATGATATCTTCTCTGTATGAGTTGAGGAAAA	320
OY	844	gtttaaagagaaagsggtactaatctgtctctggaatatactcgtgagttgtgaagttgag	903
Db	321	GCTTATATGGGGCAAGAGATATCTCATTTGCTTGTGATGATATGTGGATTTGTATGGCATGG	380
OY	904	atggsggtgagaaagatgcttttccaaactggaagaacaatgycagggagtcgtaaatcgttgacta	963
Db	361	ATGACTTTAAAGGCTTTCCCTTTCCAGATTCGCGAAATAGAAAGCA--GAAATGATGATACAA	437
OY	964	cccgatgaatgaagctgtgttctgtcgtggtgtagaagaatttcttctcgtcggaatgagt	1023
Db	438	CTCGACTTGAGAGAAATGGGGCAACAGTCACATGCCATTCATCTTATTTCTTTCGCT	497
OY	1024	tcaatgatcaaatgatgagatgtgagcttcttcttcaaaagtccagcatlittcaagtgaagcat	1083
Db	498	TCCCTCACAAAGAAAGAGAGTTGTGAAATGTTTCCAAAAAANAATGTTTAAATAAAGGAAGATT	557
OY	1084	tacacatgatagttcggagactgttggaaagcaaatccgcagatgaatgtcaacggtttaccac	1143
Db	558	TCCCCCTCGAATACAAAGATGTGAGTCCGAGCGAGTTCGACAAAATAAGCAAGAGACTGCCCC	617
OY	1144	taacatattgctggtgtg 1161	.
Db	618	TATGCTGTGCTTTGGGTG 635	

RESULT	5	
BM411546		
LOCUS	669 bp	mRNA linear EST 22-JAN-2007
DEFINITION	E87586873 tomato breaker fruit lycopersicon esculentum cDNA clone	
ACCESSION	cl18G57123 5' end, mRNA sequence.	
VERSION	BM411546	
KEYWORDS	BM411546.1 GI:18263176	
SOURCE	EST.	
	tomato.	

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 669)	Alcala, J., Vrehlov, J., White, R., Viston, T., Karamycheva, S. A., Tsatni, J., Bougri, O., Kirkness, E., Utterback, T., Van Aken, S., Roming, C. M., Fraser, C. M., Martin, G. B., Tanksley, S. D., and Giovannoni, J.	Generation of ESTs from tomato fruit tissue, breaker stage (2002)	Unpublished (2002)	Contact: CUGI

**FEATURES**  
**source**

Seq primer: T3.

Location/Qualifiers

1. 669

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/organism="Lycopersicon esculentum"
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/cultivar="TA496"

/abb\_xrei="laxon:4081"

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/clone=CLEG3/123"
/c]one ]ib="tomato breaker fruit+R
```

```
/crtone_id= comaleo di  
/tissue type="Pericard
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```
/dev_stage="brea
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```
/lab_host="SOLR"
```

```
/note="Vector: p
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Site\_2: xhoI; supplier: Boyce Thompson Institute;

sequencing: The Institute for Genomic Research. From

lycophene accumulation on the blossom and of fruit) were harvested at the breaker stage (first sign of

were cut in half and the seeds and locules were discarded.

	prior to freezing the pericarp.			
BASE COUNT	187 a	119 c	136 g	227 t
ORIGIN				

Query Match	4.1%	Score	126.2	DB	10	Length	669
Best Local Similarity	55.6%	Pred.	No. 2.4e-17				
Matches	242	Conservative	0	Mismatches	193	Indels	0
						Gaps	0

QY	2331	ccagtgacatctcaagtcgaagaagctttccgcaagctccagaagcttgaagttgtaa	2350
Db	83	ccatttgattcttccctctctaggtacatttccgagaaccttaagaaagcttagctttttaga	142

QY 2391 agacatctacctaagctggtcactccttgacacatcatagctgaagtgcctaacctcttaggtg 2450  
 |||||  
 Db 143 GGTACTCGGTTGATTTGGAGGATTTTGGAGATCTTGGTAAGTTGGCCCTAAACCTCAGGCC 202  
 |||||

QY	2451	203	Db
	ctgaagcgcgatgtagtcagcctgtgttgtagaagaatgagccatcgttaaggatt	2510	
	ctttaaactagatgatgacccctccattgcttactgatttgggaagtagggcaagagccttt	262	

QY 2511 aatcgattgaagcgttttgcctaataataatagtttcccaagtcctggaagccacaat 2570

Db 263 CCACACTTGAAGTCTTCCGATGAGCATTATCTTCATGATGATGATAGCATGATGT 322

Qy 2571 gacaaatttcctcgttccttgagcgccctcattgataagaattgtcaaaaatttgaaaagata 2630  
Db 323 gattcattttccacgaccttgaaacacactatgctcatttaaccgtttgttgagacatgtrtttcgattc 382

QY	2631	cccatbtagttgcagagatacacacacactacagctgattgtagtaagaagagtgctcc	2690
Db	383	ccacagcactttgtagacataaacacactcttcacctgattcatctaaagacctgcaaa	442

QY	2691	aaactctgggaactctgctgcacgaattcagaagaacaagaahcctctggaacaaccc	2750
Db	443	tcctgtttgggaactccgccaaagatgatctcagcaggaataattgaaacacactatgcgaattct	502

Qy	2751	gtgagatgttcgcatc	2765
Db	503	gttgagagctctgctatc	517

RESULT 6  
BE473157

[illegible]

ORGANISM	Solanum tuberosum
SOURCE	potato.
KEYWORDS	EST.
VERSION	BE4/2137.1
GL:9303046	

REFERENCE  
1. (bases 1 to 607)  
Asteridae: easterids I; Solanales; Solanaceae; Solanum.

**AUTHORS**  
van der Hoeven, R., Bezzerides, J., Bachem, C., Horvath, B., Vissler, R.,  
Holt, I. E., Liang, F., Hansen, T. S., Uterback, T., Bowman, C. L., Doan,  
B., Bougrel, O., Buell, C. R., Ronning, C. M., Tanksley, S. D. and Baker,  
D.

TITLE  
Generation of ESTs from potato swelling stolons  
JOURNAL  
Unpublished (1999)  
COMMENT  
Contact: Research Genetics, Libraries Division  
Tel. 1-800-211-6105

FEATURES

- Email: [cdna@resgen.com](mailto:cdna@resgen.com)
- 5 prime sequence.
- location/qualifiers
- 1 c07
- Accession

```

/organism="Solanum tuberosum"
/cultivar="Bintje"
/db_xref="taxon:4113"
/clone="CSTA3606"
/clone_l1b="potato stolon, Cornell university"

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/tissue\_type="axillary buds of stem explants, swelling stolons"  
 /dev\_stage="1 to 3 days"  
 /lab\_host="SOLR"  
 /note="Vector: Bluescript SK(-); Site\_1: EcoRI; Site\_2: XhoI; RNA was supplied by Christian Bachem & Beatix Horvath(Laboratory of Plant Breeding, Dept. of Plant Sciences, Wageningen University, The Netherlands). Total RNA was isolated from developing axillary buds of potato nodal stem cuttings cultured on medium for the introduction of tuber formation as described in Bachem et al. (Plant Journal 1996). Tissue samples were taken of stages corresponding to growing stolons and the early stages of tuber formation."

BASE COUNT 192 a 81 c 151 g 183 t  
 ORIGIN

Query Match 4.0%; Score 125.4; DB 10; Length 607;  
 Best Local Similarity 54.2%; Pred. No. 3.5e-17;  
 Matches 302; Conservative 0; Mismatches 246; Indels 9; Gaps 2;

QY 849 aagagaagaaggaacttaattgtcttgatgatactgagtgatgagtgatgagc 908  
 DB 15 AAAGGAGAGATGCTCATGTTGTTAGATGTTGGTAGCAGAGATCATGATGAT 74  
 QY 909 gtgagagagatgcttcaactgagacatgacgagagtgatgacatgcttgaacct 968  
 DB 75 GTTAAAGAAAGTTTTCGCA--GAAACAAAAGGGGTATGCAATCATGATGATGACGCGT 131  
 QY 969 aatgatgaagtgatgctgtgtagagaaatttcttgcgagtgatgctcatg 1028  
 DB 132 GATGATATGCTAGTACTTATGCAATACAGAACCTCATGATC-----TCAATTTCTTG 185  
 QY 1029 gataaagatgagagtgagagcttcttcaaaagtgacagatcttcaagtgaaacat 1088  
 DB 186 AATGGAAGAAAGTGTGAAATGTTGTAAGAGAGAGTGTGCAAGGAGGTGTCCT 245  
 QY 1089 taatgagtcgagagctgttgaagaagaatgcagatgaaatgctgcggttaccctact 1148  
 DB 246 GATGATTAATGTTGAACTTGGAAAGAAATGTCAGGAAATGTTGGTAGTACCTGCT 305  
 QY 1149 atgtgtgtgtgtgagagcttcttcaaaagtgacaaatgagaaatgtaaacatgct 1208  
 DB 306 TTAGTGTGTAATGTCAGAGAGGTTAAAGAGTGTGTCGAATCAATGATGCTTAAGGTT 365  
 QY 1209 gctaaagatgctcaatgcttcttcaaaatgacatgcttcaagtgatgctt 1268  
 DB 366 CAGAAAATGTGCGAGAGCATTTTATTAATAAATCAAGAGGCTGCTTGAATTTGTA 425  
 QY 1269 ggggttgatgacatgcttgaagaagaatgcttcaaaatgcttcttgcatttcggaatt 1328  
 DB 426 GAGATGAGTTACATGCTTGGCTCAGAGAGTACAGACGCTTTTGTACTGGGCTGCT 485  
 QY 1329 ttccagaagaacagtgatattccatgagaatgttgaatgacatgagtgatgagtg 1388  
 DB 486 TTTCCTTCGAGGCTTGTGATACCTTCTTGGAAATGATGCTTGTGATAGCGGAGG 545  
 QY 1389 ttccgagagtgagaa 1405  
 DB 546 TTAAATAAGCTTCACAA 562

RESULT 7  
 BI934806 659 bp mRNA linear EST 18-OCT-2001  
 LOCUS BI934806  
 DEFINITION EST54655 tomato flower, anthesis Lycopersicon esculentum cDNA  
 ACCESSION BI934806  
 VERSION BI934806.1 GI:16249278  
 KEYWORDS EST.  
 SOURCE tomato.  
 ORGANISM Lycopersicon esculentum

## REFERENCE

## AUTHORS

van der Hoeven,R.S., Bezzerides,J.L., Karamycheva,S.A., Tsai,J.,  
 Uiterback,T., Van Aken,S., Ronning,C.M., Nierman,W., Fraser,C.M.,  
 Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.  
 Generation of ESTs from tomato flower tissue, anthesis (2001)  
 Unpublished (2001)

## JOURNAL

## COMMENT

Clemson University Genomics Institute  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Email: <http://www.genome.clemson.edu/orders/index.html>  
 This clone is available through the Clemson University Genomics  
 Institute  
 Seq primer: T3.

FEATURES  
 source  
 location/Qualifiers

1..659  
 /organism="Lycopersicon esculentum"  
 /cultivar="TA496"  
 /db\_xref="taxon:4081"  
 /clone="CTOD20N16"  
 /clone\_lib="tomato flower, anthesis"  
 /tissue\_type="flower"  
 /dev\_stage="anthesis"  
 /note="Vector: Bluescript SK(-); Site\_1: EcoRI; Site\_2: XhoI; supplier: Corneli University; sequencing: The Institute for Genomic Research; Flower buds and flowers were taken from greenhouse plants (4-8 wks old, TA496). They were immediately frozen in liquid nitrogen and then size-separated while remaining frozen."  
 BASE COUNT 205 a 100 c 157 g 197 t  
 ORIGIN

Query Match 3.9%; Score 122.2; DB 10; Length 659;  
 Best Local Similarity 55.9%; Pred. No. 1.8e-16;  
 Matches 345; Conservative 0; Mismatches 248; Indels 24; Gaps 5;

QY 951 atactgttgaactaccgtaatgataagtgatgctgtatgctgtgtagagaatttct 1010  
 DB 1 ATTAATTTGACTAGTAGGCAAGAGAGGTGCTAGTATGAGATCCCGATAGCAATCCT 60  
 QY 1011 ttgcgagatgagcttcaatgataagatgagagtgtagagcttcttcaaaagtgcagcat 1070  
 DB 61 CATTAATAATGAACCTTTAAACTTGTGATATGTTGGAAGTTAATCCGACAGAGTGT 120  
 QY 1071 tcaagtgaa--gcatcaccatgagtgatgagagctgttgaagaagaatgcagatgaa 1127  
 DB 121 GGGGTAAACATGATGCTGCTCTGATGTGAGAGATATGAGAACAAATGACCAAGA 180  
 QY 1128 tgtcaggggttaccaactaactatgtcgtgtgtagagagcttc--aaatcctaaagg 1184  
 DB 181 TGCCAAAGAGCTGCCCTTAGCTCTTCTAGTACGGGACATCTCTTAATAATTTTCAGA 240  
 QY 1185 acaatagaagaatgaaacagtgcttaagaatgataagatccttcgttcaaaatgagcct 1244  
 DB 241 ACACGAGAAAGTTGGAACGAGTGTTCAAAAGTGTAAAGTTGTTGCTGATGAATCA 300  
 QY 1245 gatgaagatgttcaagtgctgtgtgtgtagtgaactgacacatgcataaa 1304  
 DB 301 GATAT---ATGCTAGAGAGTCTGCTGATAGTATGATTAATTAACCTGATGATCA 357  
 QY 1305 acatgtctctgtcatcttgcgaatttccagaagaacagtgatattccagtgagaatttg 1364  
 DB 358 CCATGTTCCCTTACATGAGGAGGCTTTCGCCGAAGACAGTGTGTTAACAATGTTAGATTG 417  
 QY 1365 atgagatcagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 1424  
 DB 418 ATCACTTATGATGATTTGAGGAGGTTTATATACAGATGAATTAATGCGAGAG----- 469

QY	1425	gagaaagtggttgcgaagcctgtctgatgatgatgctagctccctccgcacgaagaagatcga	1484
Db	470	-----ATTGTATGAGAGCATCTTGTTAAGCAGAGAAATCTGGTAATGTTAGAAACAGCAGTTT	525
QY	1485	gatggaacaaatatagtatcgttaaggttcaatgatcatatataatagacctgtgcgtgaga	1544
Db	526	AATGG---CGAGACAAAACATGTCGTGTCCATGATCGATTCGATTTGATTTTAAGA	582
QY	1545	gaagttcaaggagagaa	1561
Db	583	AGAGCCGAGAAAAGAGAA	599
RESULT	8		
LOCUS	BE923412	426 bp	MRNA
DEFINITION	EST427181 potato leaves and petioles Solanum tuberosum cDNA clone		
ACCESSION	CSRB2414	5' sequence, mRNA sequence.	
VERSION	BE923412		
KEYWORDS	BE923412.1	GI:10449488	
SOURCE	EST.		
ORGANISM	Solanum tuberosum		
REFERENCE	van der Hoeven,R.S., Bezzerides,J., Holt,I.E., Liang,F., Cho,T., Utterback,T., Hansen,C.L., Doan,B., Bougri,O., Buell,C.R., Ronning, C.M., Fry,W.E., Tanksley,S.D. and Baker,B. Generation of ESTs from potato leaves and petioles unpublished (2000)		
TITLE	Journal		
COMMENT	Contact: Cathy Ronning The Institute for Genomic Research For clone request: Please contact Research Genetics, Libraries Division tel 1-800-711-6195, email cdna@esgen.com.		
FEATURES	source		
	1..426		
	/organism="Solanum tuberosum"		
	/cultivar="Kennebec"		
	/db_xref="taxon:4113"		
	/clone="CSRB2414"		
	/clone_lib="potato leaves and petioles"		
	/tissue_type="leaflets and petioles"		
	/dev_stage="8 weeks old plants"		
	/lab_host="SOLR"		
	/note="vector: pBluescript SK(-); site_1: EcoRI; site_2: XhoI; Tissue was supplied by Dr. Fry (Cornell University). Leaflets and petioles were isolated from 8 week old greenhouse grown plants. The plants were watered and fertilized freely. The tissue was immediately frozen in liquid nitrogen."		
BASE COUNT	130 a	76 c	102 g
ORIGIN		118 t	
Query Match	3.9%	Score 120.4	DB 10; Length 426;
Best Local Similarity	58.5%	Pred. No. 4.4e-16;	
Matches 261; Conservative	0;	Mismatches 161;	Indels 24; Gaps 2;
QY	606	gggagaccacaagatcatcccgatttcgagatcgagagagcatgtaaaacaaccttga	665
Db	1	GGGGAACTTAGAAGTTGTCTCATTCGTAGGAGATGGGAGCGATCGGGAACAAACACTTTGGCT	60
QY	666	aaagaagttacaatgataatcaattctatgacgattttatgtcgaagcctgggctacc	725
Db	61	ACAAAACCTTAGTCATCTGTGCATTATAGTTCGATTTGATTTTCGTCCAAAACCAACT	120
QY	726	atactcacacagcacacaacaaagaagaatttgcgcgggccttcgcatcacacaatcaa	785
Db	121	GTTTTCACAAAGATATTGTGTGAGAAATGATCTCAAGGCGCTTCTTTTGGACAAAGTGA	180
QY	786	atgatatgacaaggttaagatgatggtgtgaagcagagctagacagacatglttacagaaagt	845

Db	181	GAACCTGATA-----ATCAGCTAGCGGACCGCATCTCCAAAGCAT	219
QY	846	ttaaaggaagaagtgacttaattgtcttgatgatatactcggagttggaagtgtagat	905
Db	220	CTGAAGACGACAGATATCTTGCTGATCTTTCATGACATATGACTACGAAAGCTTGGAT	279
QY	906	ggcgtgagacgatctctccacactgaagacaaatgcagggagtcgaatactgttactacc	965
Db	280	GATATTAACATCATGTCTTCCCA---GACTGTATTAATGAACAGCAAAATCTCTGACTACT	336
QY	966	cgtaatgatgaagtactgttctatgcctggtgtgaagaatttttttggcgagtagctc	1025
Db	337	CGGATGTGGAAGTGGCTGGAATATGCTAGTTCAGGTAAAGCCTCCTCATCATATGGGCTC	396
QY	1026	atgatacaaatgagatgtagtgcctc	1051
Db	397	ATGAATTTTGACGAAGTTGGAATTT	422
RESULT	9		
LOCUS	AO367206	701 bp DNA linear	GSS 07-MAR-2000
DEFINITION	tox00002A12r CUGI Tomato BAC library Lycopersicon esculentum		
ACCESSION	AO367206		
VERSION	AO367206.1	GI:4221674	
KEYWORDS	GSS.		
SOURCE	tomato.		
ORGANISM	Lycopersicon esculentum		
REFERENCE	Eukaryote; Virdidiplantae; Streptophyta; Embryophyta; Tracheophyta;		
AUTHORS	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
TITLE	Asteridae; euasterids I; Solanales; Solanaceae; Solanum;		
JOURNAL	Lycopersicon.		
MEDLINE	1 (bases 1 to 701)		
COMMENT	Budiman,M.A., Mao,L., Wood,T.C. and Wing,R.A. A deep-coverage tomato BAC library and prospects toward development of an STC framework for genome sequencing Genome Res. 10 (1), 129-136 (2000)		
FEATURES	Source		
FEATURES	location/qualifiers		
SOURCE	1..701		
	/organism="Lycopersicon esculentum"		
	/cultivar="Heinz 1706"		
	/db_xref="taxon:4081"		
	/clone="tox00002A12r"		
	/clone_lib="CUGI Tomato BAC library"		
	/tissue_type="Nuclei preparation from leaf"		
	/lab_host="E. coli DH10B"		
	/note="Vector: pzeoBAC 11; Site.1: HindIII; Site.2: HindIII; Tomato is a vegetable crop that ranks second only to potatoes in value and importance. Among plant geneticists and physiologists, tomato represents an ideal dicot model beside Arabidopsis and monocot rice to derive genomic information from. To facilitate the genome analysis of tomato, we have constructed a tomato BAC library that is suitable for positional cloning, physical mapping, and genome sequencing. The library contains 129 ,000 clones and a random sampling of 498 clones indicated an average insert size of 117.5 kb. With 15X haploid genome equivalents (1C equals 953 Mb) (Arumuganathan and Earle, 1991), the probability to recover any particular sequence is greater than 99%. High stability, large insert		



VERSION	BH142383.1	GI:15194909
KEYWORDS	GSS.	
SOURCE	tomato.	
ORGANISM	Lycopersicon esculentum	
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae: euasterids I; Solanales; Solanaceae; Solanum;	
AUTHORS	Lycopodium.	
TITLE	1 (bases 1 to 639)	
JOURNAL	van der Hoeven,R., Sun,H., Cho,J., Uterback,T., Konning,C. and Tanksley,S.	
COMMENT	Tomato Demethylated Genomic DNA Sequences Unpublished (2001) Contact: CUGI Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Email: http://www.genome.clemson.edu/orders/index.html tomato demethylated genomic DNA Insert length: 1270 Std Error: 0.00 Seq primer: M13F-R Class: shotgun.  Location/Qualifiers 1..639 /organism="Lycopersicon esculentum" /cultivar="E6203" /db_xref="taxon:4081" /clone="cTOG24C17" /clone_lib="cTOG" /issue_type="Young leaves" /dev_stage="12-14 weeks post harvest" /lab_host="E.coli JM109" /note="Vector: pBluescript SK(-). Site.1: EcoRI. Site.2: XhoI. This library was made from short EcoRI digested fragments of the genome of Lycopersicon esculentum ligated into pBS (SK-). The fragments were cloned into the methylation restrictive E.coli strain JM109 with the purpose of enriching the library for non-methylated DNA fragments. This procedure may enrich the pool of cloned fragments in JM109 cells for sequences representing expressed genes. Average insert size 1.27 Kb."	
BASE COUNT	188 a	104 c 150 g 197 t
ORIGIN		
Query Match	3.8%;	Score 118; DB 12; Length 639;
Best Local Similarity	52.0%;	Pred. NO. 1.5e-15;
Matches 319; Conservative	0;	Mismatches 285; Indels 10; Gaps 2;
OY 960 actaccgtaatgatgaagtagctgttatgcgttggtgtagagaattttcttcggagatg 1019		
Dd 9 ACTGGCGTCAAGATATTGTTCGATTATATGCAGTTGTCTCGTTTTCCGCCCTCATATGAAG 68		
OY 1020 agcttcagtcaagaatgaagagcttgcgttatgcgttggtgtagagaattttcttcggagatg 1079		
Dd 69 TCTTTCTTAAGTGTACAAAGATAGTTGGATCATATTCACCAAAAAATTATTCAAAACAAT 128		
OY 1080 gcattaccataatgaatcgagacgttgttgaagaagcaaacgcagagatgaatgcaggatta 1139		
Dd 129 CCGTGTCCTCTCTTTAGAAAAAAGGGGAGACGATATTGTGTAACAATGTCAGAGATT 188		
OY 1140 ccactaaactatgcttggttgcaaggaccttccaactctaagaagaacaatagaagattgg 1199		
Dd 189 CCCCTCGGTTGTGTTGTTGCTGTGACTGTTGTGAAAAATGGACCACACATGATTAAT 248		
OY 1200 aaaactctgtcaagaatgcatcaatcgtgcacaaatgacctgtagaagcatgttca 1259		
Dd 249 TGGAAGAAGGTTTAGGAAAAATCTGAGCTCGTTCTTTGGTACTGTGCTGAACGATGCCAA 308		
OY 1260 cgtytgcttggttgtagtagatgaactgaagaagcagctgtaaaaacatgtcttcgat 1319		
Dd 309 TCAATTTCTCTGTGAGCTACAAATTATTTGGCCCCAATATTTTAAAGCGTTGTTCTCTAT 368		

QY	776	cacaatcaaatgataagcagggttaagaatgttggaagcagagctagcagacatgtt	835
QY	1320	ttcggaatttttcgaagaacgtagatattccagtgaaagatttgaatgacatgagtg	1379
Db	369	CTTGGAGGCTTTCCTGGAAGATATGAGCAATTGATCTTTCCAACTGTGTTGGCTATGACTT	428
QY	1380	gctgaggggttccctgaagcttggaaaatgat-----ttggaaggaagaggttgagaagtgct	1433
Db	429	GCTGAGCAATTCGTATTAAGGCAAGAAGCAATTAAGAGATTAGAAGTGTGGCGAGGAGTAT	488
QY	1434	ttgcaagagcttgtcgatagatgtttagtctctgcgcgaagaagagtcgagatgaaaca	1493
Db	489	GTAGAAGGCTTAATGTATGATGATGAAGTCTAAT--TTTGGCTGGTGAACAAGGCTAATGCA	544
QY	1494	aaattagatcatcgaaggttcattcatcatataataatataatgacctgtgcgtgagagaagttaca	1553
Db	545	AGGATGAAAGTGTGCAAAATTCACGATCTTCTTCCCAAAATGTGCTTAAGGAAACCTCA	604
QY	1554	aggagagaacatttt	1567
Db	605	ACTGAAATGTGTG	618
RESULT	12		
BEA60726/c			
LOCUS	BEA60726	617 bp	mRNA linear EST 18-MAY-2001
DEFINITION	EST412145 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA clone CLE36A22, mRNA sequence.		
ACCESSION	BEA60726		
VERSION	BEA60726.1	GI:3505028	
KEYWORDS	EST.		
SOURCE	tomato.		
ORGANISM	Lycopersicon esculentum		
	Eunaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;		
REFERENCE	1 (bases 1 to 617)		
AUTHORS	Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E., Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Roming,C.M., Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.		
	Generation of ESTs from tomato fruit tissue, breaker stage unpublished (2000)		
TITLE	Unpublished (2000)		
JOURNAL	Contact: CUGI		
COMMENT	Clemson University Genomics Institute 100 Jordan Hall, Clemson, SC 29634, USA Email: <a href="http://www.genome.clemson.edu/orders/index.html">http://www.genome.clemson.edu/orders/index.html</a> 5 prime sequence.		
FEATURES	Location/Qualifiers		
SOURCE	1..617		
	/organism="Lycopersicon esculentum"		
	/cultivar="TRA96"		
	/db_xref="taxon:4081"		
	/clone="CLEG36A22"		
	/clone_lib="tomato breaker fruit, TIGR"		
	/tissue_type="Pericarp"		
	/dev_stage="breaker"		
	/lab_host="SOLR"		
	/note="Vector: pBluescriptsmcMudapt; Site_1: EcoRI; Site_2: XhoI; Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of the fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."		
BASE COUNT	162 a	148 c	100 g 207 t
ORIGIN			
Query Match	3.6%	Score 113;	DB 10; Length 617;
Best Local Similarity	51.1%;	Pred. No. 1.9e-14;	
Matches	291; Conservative	0; Mismatches 275;	Indels 3; Gaps 1;

Db 586 CACCATGGAGACTGATGATTTGGAAAGATGATGAAGAGATCTAGAAAAACCACT 527

QY 836 acagaaagtttaagaaagaggtacttaattgtcttgatgatatctgagttgtga 895

Db 526 TCGTGTCTTTAAAGAAAGCAAAATACCTTGCTGGTGTGATGATGCTCGCAAAAGAGA 467

QY 896 agtggtagaggtgtagagagatgcttccaaactgaaagaaagagagagtcgaact 955

Db 466 AGCATGGAGAGTTTGAAGAGACATCCCGATGACAAAGAT---GGACAGAGATCAT 410

QY 956 gtgactaccggaatgatgaagtagctgtgtatgctgtgtgtagaattttcttgcg 1015

Db 409 TATTACACGCGCAAGAGATATGCTGAAGAGCGACGCGAGAGAGCTTTGTTCATTA 350

QY 1016 gatgagttcatgtagcaagatgaggttgagttctttaaagaagtcagactttcaag 1075

Db 349 ACTGCTGTTCTTAAGTCAAAGAAAGAGTTGGATCTCTTCTTGAAGAACTACTGTATGT 290

QY 1076 tgaagcatcacatgagttgtagagactgtgtgaaagcaatcgacatgtagtcaag 1135

Db 289 TCGAGCAATGTTGCAGAAATGGAAGCTTACCTAAGATATGTTGGAAGAGTGAAGG 230

QY 1136 gtaccactactactgtgctggttgcaaggtcttcaactcaaaagagacaatagaaga 1195

Db 229 TTTACCTCTGCAATTTGTTGATTTAGCGGACTACTTTCGATTAAGAAAGATCTAGATGA 170

QY 1196 ttggaagaactgtgcaagaatgtagtcaatctcgtcacaaatgtagtctgtagaagatg 1255

Db 169 ATGGCAAAAGGTAAAGATACCTTTGGAGAGACATTAAAGAAATTAATCTGTGAAAT 110

QY 1256 ttaactgtgctggtgtgtagtagtcaacttgacaagagcagcctaaagaactgtctc 1315

Db 109 CTCGCAACATCTACTACAGTCAAGTCAATGATTTGTCAATTGAGCTCAAGCAGTCTTCT 50

QY 1316 gcaattcggaattttccagaagacagtg 1344

Db 49 CTACTTGTGATGTTCCAGAGATCGAG 21

RESULT 13

LOCUS BM408141 756 bp mRNA linear EST 22-JAN-2002

DEFINITION EST582468 potato roots Solanum tuberosum cDNA clone cPRO33620 5'

ACCESSION BM408141

VERSION BM408141.1 GI:18259771

KEYWORDS EST.

SOURCE potato.

ORGANISM Solanum tuberosum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

REFERENCE 1 (bases 1 to 756)

AUTHORS van der Hoeven,R., Sun,H., Karamycheva,S.A., Tsai,J., Van Aken,S., Utebback,T., Chimingo,A., Bougri,O., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B.

Generation of ESTs from potato roots

Unpublished (2001)

Contact: Research Genetics, Libraries Division

Tel: 1-800-711-6195

Email: cdna@resgen.com

For clone info: please contact Research Genetics, Libraries Division tel: 1-800-711-6195, email cdna@resgen.com

Seq primer: T3.

FEATURES

source

1..756

Location/Qualifiers

/organism="Solanum tuberosum"

/cultivar="Kennebec"

/db\_xref="taxon:4113"

/clone="cPRO33620"

/clone\_lib="potato roots"

/tissue\_type="roots"

/dev\_stage="in vitro grown stem cuttings"

/lab host="SOLR"

/note="Vector: pBluescript SK(-); Site.1: EcoRI; Site.2: XhoI; supplier: Cornell University, Tanksley lab; sequencing: The Institute for Genomic Research. Roots were isolated from in vitro grown stem cuttings on CM medium. Roots were isolated two weeks after placing the stem cuttings from in vitro grown plants on medium."

BASE COUNT 229 a 150 c 166 g 211 t

ORIGIN

Query Match 3.5%; Score 108.4; DB 10; Length 756;

Best Local Similarity 52.7%; Pred. No. 2e-13;

Matches 235; Conservative 0; Mismatches 211; Indels 0; Gaps 0;

QY 2353 aagctttccaagcagctcaagaagttgaaagttgaaagaactatcgaactgagcatt 2412

Db 260 ATGCACCTCCAGAGAAATCTTAAGAAAGTTAACTTGAACCTTCACCTACTTGCCATGGGAGA 319

QY 2413 acttgacatcatagctgagttgcttaaccttgaggtgctgaagctgtagatgagcct 2472

Db 320 GATAGCCCTCTCTTTGTAGATTACCGAATCTCGAGTACTTAACCTAAGAAATATGCTT 379

QY 2473 gtgtgtgaaagatgagcaccatgttlatgagatlaacgattgaagcttgcataa 2532

Db 380 TCACAGTCCAAAGTGGGAACAACTGMAAGAGGGGCTTGCTTTAAACTATGCTGA 439

QY 2533 ttaataagtttctcaagttctgaaagcacaatgacaatttccgtctgagc 2592

Db 440 TTGAGATATCTGATATTAACACTGAGTGGAGTGCCTTAATGATCATTTCCGCTGGAAC 499

QY 2593 gccctcagatgagaagttgcaaaattgaaagagataccatgagttgcagataac 2652

Db 500 ATCTAGTTCTTAAGAGTTGCTTTCACCTTGACACATCCCTCAGATCTGGGAATATTC 559

QY 2653 acaactacacgtgattgagttaaagagtgctccccaacttgagggaactgctgac 2712

Db 560 CGACTTTGCAGATATATGAGCTGGAAATTCACCACTATGCAAGTCTTCACCTAAG 619

QY 2713 gaattcagaagaagaagacactcggaacacacttgtagtctgtctccaatc 2772

Db 620 AGATCCCAAGAGGACACCAAAATGATGCTAAGCAAACTGTAAGTGGATGAGAGAA 679

QY 2773 cattgaagagagtgatctgattca 2798

Db 680 ATTTCGGAGATTAATGCTGTTCCA 705

RESULT 14

LOCUS AM030063 417 bp mRNA linear EST 18-MAY-2001

DEFINITION EST273318 tomato callus, TMU Lycopersicon esculentum cDNA clone

ACCESSION AM030063

VERSION AM030063.1 GI:5888819

KEYWORDS EST.

SOURCE tomato.

ORGANISM Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.

REFERENCE 1 (bases 1 to 417)

AUTHORS Alcala,V., Vredalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Upton,J., Craven,M.B., Bowman,C.D., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.

Generation of ESTs from tomato callus tissue

Unpublished (1999)

Contact: CUGI

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>









GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 11, 2002, 11:42:09 ; Search time 156.24 Seconds  
(without alignments)  
4872.108 Million cell updates/sec

Title: US-09-864-680-2

Perfect score: 3099  
Sequence: 1 caaatattcttgagtgagta.....tttagtttaaaaaaaaaa 3099

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA :  
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3: /cgn2\_6/prodata/2/ina/5A\_COMB.seq:\*  
4: /cgn2\_6/prodata/2/ina/5B\_COMB.seq:\*  
5: /cgn2\_6/prodata/2/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/prodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3099	100.0	3099	4	US-09-360-186-2
2	2725.6	88.0	31491	4	US-09-360-186-1
3	2718	87.7	2718	4	US-09-360-186-4
4	172.2	5.6	5475	2	US-08-680-327-1
5	172.2	5.6	5475	4	US-09-228-246-3
6	170	5.5	10968	2	US-08-680-327-2
7	170	5.5	10968	4	US-09-228-246-1
8	164.2	5.3	5134	2	US-08-310-912A-157
9	164.2	5.3	5134	4	US-09-301-085-157
10	164.2	4.8	5134	5	PCT-US95-04589-157
11	149.2	4.8	3997	3	US-08-947-823-2
12	149.2	4.8	51952	3	US-08-947-823-1
13	147.6	4.8	3982	3	US-08-947-823-4
14	83.6	2.7	4465	3	US-08-930-996A-3
15	72.6	2.3	7218	1	US-08-232-463-14
16	56	1.8	4946	3	US-08-930-996A-1
17	47.2	1.5	3925	4	US-09-330-330-2
18	42.8	1.4	289	4	US-09-007-005-17
19	42.8	1.4	289	4	US-09-244-796-17
20	42	1.4	10332	4	US-09-330-330-3
21	41	1.3	2353	4	US-09-004-838-2
22	39.4	1.3	503	4	US-09-004-838-134
23	38.4	1.2	1036	4	US-09-004-838-3
24	37.8	1.2	1426	4	US-08-858-207A-98
25	37	1.2	1652	4	US-09-004-838-6
26	36.6	1.2	4163	4	US-09-004-838-70
27	36.6	1.2	4208	4	US-09-004-838-1

28	36	1.2	1902	3	US-09-041-991A-7	Sequence 7, Appl
29	36	1.2	5720	4	US-09-442-100-1	Sequence 1, Appl
30	35.8	1.2	1038	4	US-09-004-838-128	Sequence 128, App
31	35.4	1.1	732	4	US-08-998-416-1036	Sequence 1036, Ap
32	35.2	1.1	1872	3	US-09-041-991A-5	Sequence 5, Appl
33	35.2	1.1	51259	3	US-08-781-891-209	Sequence 209, App
34	35	1.1	3147	4	US-09-066-046-1	Sequence 1, Appl
35	35	1.1	7218	1	US-08-232-463-14	Sequence 14, Appl
36	34.8	1.1	1739	3	US-08-714-918-1	Sequence 1, Appl
37	34.8	1.1	1739	4	US-09-265-315-1	Sequence 1, Appl
38	34.8	1.1	1739	4	US-09-265-315-1	Sequence 1, Appl
39	34.8	1.1	1739	4	US-09-266-417-1	Sequence 1, Appl
40	34.6	1.1	277	4	US-09-007-005-3	Sequence 3, Appl
41	34.6	1.1	277	4	US-09-244-796-3	Sequence 9, Appl
42	34.4	1.1	1902	3	US-09-041-991A-9	Sequence 9, Appl
43	34.4	1.1	6152	3	US-08-973-462-1	Sequence 1, Appl
44	34.4	1.1	51952	3	US-08-947-823-1	Sequence 1, Appl
45	34.2	1.1	1096	4	US-09-004-838-132	Sequence 132, App

## ALIGNMENTS

RESULT 1  
US-09-360-186-2  
; Sequence 2, Application US/09360186  
; Patent No. 6262343  
; GENERAL INFORMATION:  
; APPLICANT: Staskawicz, et al.  
; TITLE OF INVENTION: B2 Resistance Gene  
; FILE REFERENCE: 50687  
; CURRENT APPLICATION NUMBER: US/09/360,186  
; CURRENT FILING DATE: 1999-07-23  
; EARLIER APPLICATION NUMBER: 60/093,957  
; EARLIER FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 3099  
; TYPE: DNA  
; ORGANISM: Capsicum annuum  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (93)..(2810)  
US-09-360-186-2

Query Match	100.0%;	Score 3099;	DB 4;	Length 3099;
Best Local Similarity	100.0%;	Pred. No. 0;		
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RESULT      2
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: Sequence 1, Application US/09360186
: US-09-360-186-1
: Patent No. 6262343
: GENERAL INFORMATION:
: APPLICANT: Staskavicz, et al.
: TITLE OF INVENTION: Bsz Resistance Gene
: FILE REFERENCE: 50687
: CURRENT APPLICATION NUMBER: US/09/360,186
: CURRENT FILING DATE: 1999-07-23
: EARLIER APPLICATION NUMBER: 60/093,957
: EARLIER FILING DATE: 1998-07-23
: NUMBER OF SEQ. ID NOS: 9
: SOFTWARE: PatentIn Ver. 2.0
: SEQ. ID NO. 1
: LENGTH: 31491
: TYPE: DNA
: ORGANISM: Capsicum annuum
: US-09-360-186-1

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Db 1741 ctcaaaagtcgtgagctgagacacagacagattgtgttccctcagagataactaagc 1800  
QY 1893 ctcatctgtgtgaggtactcatctgttccagctatgggaatttcogatgtacctccagaa 1952  
Db 1801 ctcatctgtgtgaggtactcatctgttccagctatgggaatttcogatgtacctccagaa 1860  
QY 1953 atttgcaggttatggaattctgcagacattcatctgttcaacaggttccgatacataata 2012  
Db 1861 atttgcaggttatggaattctgcagacattcatctgttcaacaggttccgatacataata 1920  
QY 2013 atttctgcaggaatttgggaacttgaactaagtcgaattgaagcattccaagatt 2072  
Db 1921 atttctgcaggaatttgggaacttgaactaagtcgaattgaagcattccaagatt 1980  
QY 2073 taattgcagaatgcccagaatggaatctgttgcacaaaggaagcacttggattttccaac 2132  
Db 1981 taattgcagaatgcccagaatggaatctgttgcacaaaggaagcacttggattttccaac 2040  
QY 2133 ttacaacattttcttactgttcccaagctgttgcacgaaggaggttatattgggaatt 2192  
Db 2041 ttacaacattttcttactgttcccaagctgttgcacgaaggaggttatattgggaatt 2100  
QY 2193 cagaatgttcaaaaaaattaggaatcagatggaataaagatgacataaagtttcgggac 2252  
Db 2101 cagaatgttcaaaaaaattaggaatcagatggaataaagatgacataaagtttcgggac 2160  
QY 2253 tcttggtctcccaacaactctgtctatctgcagcaacttgaataatgttagcttatattc 2312  
Db 2161 tcttggtctcccaacaactctgtctatctgcagcaacttgaataatgttagcttatattc 2220  
QY 2313 gttgatatgaaccttgcgcagtgatacttcaagttcgaagaagccttccagcaagcctc 2372  
Db 2221 gttgatatgaaccttgcgcagtgatacttcaagttcgaagaagccttccagcaagcctc 2280  
QY 2373 aagaagttgaagttggaagaactatctaaagctgtgatacacttgcagatcatagctgag 2432  
Db 2281 aagaagttgaagttggaagaactatctaaagctgtgatacacttgcagatcatagctgag 2340  
QY 2433 ttgcttaaccttggagctgagcgtgataagctgtgataagccttctgttgttgaagaatgcat 2492  
Db 2341 ttgcttaaccttggagctgagcgtgataagctgtgataagccttctgttgttgaagaatgcat 2400



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QY 1462 tccctgcagcaagaagtcgagatggaacaaattagatcatgtaaggttcagatc 1521
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Db 4193 TGTATGACCATGAGAGACCTAAT---ACCAAGGTGAAGACGTCGCATTCATGATTT 4249
QY 1522 taatataagccgctgcgtgagagaagttcaaaaggagacatttatcatgaacgaca 1581
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Db 4250 TGTTCATTAATTCGTGATGGAAGGCAACAGAGATTTTCTTCTCAATCAATA 4309
QY 1582 ttgtcttgacgcat 1596
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Db 4310 GTGGAGAGGTGAT 4324

RESULT 5
US-09-228-246-3
; Sequence 3, Application US/09228246
; Patent No. 6245510
; GENERAL INFORMATION:
; APPLICANT: Staskawicz, B. S. et al.
; TITLE OF INVENTION: PRF Protein and Nucleic Acid Sequences: Compositions
; FILE REFERENCE: 51700
; CURRENT APPLICATION NUMBER: US/09/228,246
; EARLIER APPLICATION NUMBER: 08/680,327
; EARLIER FILING DATE: 1996-07-11
; EARLIER APPLICATION NUMBER: 08/310,912
; EARLIER FILING DATE: 1994-09-22
; EARLIER APPLICATION NUMBER: 08/227,360
; EARLIER FILING DATE: 1994-04-13
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 3
; LENGTH: 5475
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(5475)
; US-09-228-246-3

Query Match 5.6%; Score 172.2; DB 4; Length 5475;
Best Local Similarity 50.6%; Pred. No. 8.4e-39;
Matches 554; Conservative 0; Mismatches 523; Indels 18; Gaps 5;

QY 508 caagttcaacaacgaattttgaaggttaagaacaatagtgtgagcgtgatcaaa 567
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QY 568 ggaacaggtgttagaagatctgaagctactcttggggaacccaagttacccga 627
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Db 3302 tagatgaattaaagaaactacttggagatcaact---gagcttgatgtcatccaa 3358
QY 628 ttgtcggagtgaggagcatgtaaaaacactagcaaaaagaagttacatatgaat 687
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Db 3359 tcgttgacagccagagattgggcaagctacacacgaagaagaatttacaatgatccag 3418
QY 688 caattctacgcgttttgatgttcaatgccttgggtctacacatatcaacagcaaaa 747
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Db 3419 aagcacacctcgtctcgtatgtcatgtcgaatgtgtgtgacatcatattatcattga 3478
QY 748 aggaattttgctggcctcttgatccacaatcaaatgtagaaggtttagatga 807
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QY 868 ttgtcttgagatcatctggaagttgtgaagtgttgagatgscgtgagacgatttccaa 927
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QY 928 ctgaagacaattgcaggagtcgcaatactgttgaatcccgtaatgatgaagtgtgt 987
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Db 3653 gtgatgtttcaaatagagtagaatttccctaacaacccgttgaatgattgttcgcaat 3712
QY 988 atgtgtgtgtagaagattttcttcttgagatgagcttccatgagatcaagatgaggttga 1047
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Db 3713 atgtcaaatgtgaagtgatcccatcatctctgttattcaagagatgaagaggttga 3772
QY 1048 gtctttcaaaagtgcagacttttcaagtgaagcattacacatagatgcagactgtg 1107
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Db 3773 cattattacagaagaagctcttcaagagagaagctgtccacccgaacttgaagatgtg 3832
QY 1108 gaaagcaaatcgcagatgcatggttccacacatcatctgtgtgtgtgtgtgtgtgtgt 1167
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Db 3833 gatttgaatatcaaaaagtgttagaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3892
QY 1168 ttctcaatctaaagagacaatagaagattggaacactgtgtctaaagatttcaagtcatt 1227
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Db 3893 ttctgaacacgaagaagaagacactagattatcagaaagttagaacaagaagtcagtt 3952
QY 1228 tcgtcacaaatgacatcgtatgaacgagtgttcaggtgtgtgtgtgtgtgtgtgtgt 1287
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Db 3953 cccagagagattggcagcttgaagagagacatcatatgaattgattcaagaagaatt 4012
QY 1288 tgacaagcgtatctaaacacatgcttctgcatcttcggaatttccagaagacagtgata 1347
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Db 4013 taccacacatcttaacacctgttctctcatattttagaagattttagcaggaagaagata 4072
QY 1348 ttccagtgaaagatttgatgagacatgagatgctgtgaggggttct-----gaagtgtg 1401
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Db 4073 ttcatgtctcaaaaatgaccagagttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4132
QY 1402 aaatgatttggagagagaggttgaaggtgttgcgaagctgtgtgatgagtgctag 1461
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Db 4133 aaaaaggacaagaagataccgcacaaggttcttgcgacatctatgttgaagagtgag 4192
QY 1462 tccctgcagcaagaagtcgagatggaacaaatagatcatgaatgaatgatc 1521
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Db 4193 tgatggcatggaagaagactaat---accaagtgaaagaacgtgcgcactcatgtgt 4249
QY 1522 taatataagccgctgcgtgagagaagttcaaaaggagaaacatttatcatgaacgaca 1581
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Db 4250 tgttgataaattctgcagtagaagaaagccaaagaagatttcttccaatcaata 4309
QY 1582 ttgtcttgacgcat 1596
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Db 4310 gtggaagaagtgtat 4324

RESULT 6
US-08-680-327-2
; Sequence 2, Application US/08680327
; Patent No. 5839321
; GENERAL INFORMATION:
; APPLICANT: Staskawicz, Brian S., Oldroyd, Giles Edward,
; APPLICANT: Salmeron, John M., Rommens, Catus
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PLANT
; TITLE OF INVENTION: PATHOGEN RESISTANCE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarkquist Sparkman Campbell Leigh &
; ADDRESS: Whinston
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: MS DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/680,327
; FILING DATE: July 11, 1996
; CLASSIFICATION: 800
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/310,912
; FILING DATE: September 22, 1994
; CLASSIFICATION: 800
; APPLICATION NUMBER: 08/227,360
; FILING DATE: April 13, 1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Alan. E.
; REGISTRATION NUMBER: 35,123
; REFERENCE/DOCKET NUMBER: 5151-45038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10968 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; US-08-680-327-2

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Query Match      5.5%; Score 170; DB 2; Length 10968;
Best Local Similarity 50.6%; Pred. No. 5.2e-38;
Matches 547; Conservative 0; Mismatches 515; Indels 18; Gaps 5;

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QY 568 gaaacagttgttaagaagatctgactagaagctactctgaggaaacacagatccga 627
   || || || || || || || || || || || || || || || || || || || || ||
DB 7180 TGATGAAATTAAGATTAACACTCTGGAGATCACCT--GAGCTTGATGTCATCCAA 7236
QY 628 ttgtggagtgaggagcatagtaaaacacacttagcaaaagaagtttcaatgagat 687
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DB 7237 TCGTGGCAGCCAGGATGGGCAAGACTTACACTAGCAAGAGATTTCAATGATCAG 7296
QY 688 caatctatgcgatttgatgttcactgctgagctgagctacacatcccaagcacaacaa 747
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DB 7297 AAGTACCTCTGCTTCGATGTCATGCTCAATGCTGTGTGACTCAATATATATCATGA 7356
QY 748 aggaatcttgctgggctctctgcatccacaataaagtatgacaggttaagaaga 807
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DB 7357 GAGAGTTGTCCTCACCATTTGAAATGATGTCCTTGAGCCTTCTGATGCCAATGA 7415
QY 808 ttgggaagcagagcttaagagacatgttacagaaaagtttaagaaagaaagtaactta 867
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DB 7416 --GAAGATGCTAATAGCTGATGAGTTACGCCGATTTTGTGGCCAAAGAGATTTGGA 7473
QY 868 ttgtcttgatgatatctggaagttgtaagttgaggatgagctgagacatcttccaa 927
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DB 7474 TTCTCATTTGATGATGTTGGAGACTATAAAGTGTGGCAACAATGTATGATGCTT--CA 7530
QY 928 ctgaagacacatgcagaggtggaataactgttgaactacccgttaagtatgagctgtt 987
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DB 7531 GTGATGTTTCAATAGGAGTAAATATTCCTTAACAACCCGCTTGATGATGTCGCCGAAT 7590
QY 988 atgcggtgttagagaattttcttcgsgatagacttcaatgataagttgaggtgtga 1047
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DB 7591 ATGTCAATATGTAAAGTGATCCCATCATCTTCGTTTATTCAGAGATGACGAGATGTGA 7650
QY 1048 gtctttcaaaagttcagcatcttcaagtgaagcatctacatatagttcgaagactgtt 1107
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DB 7651 CATTTATTCAGAAAGAGCTTTTCAAGAGAGAGAGCTGTCCACTGAACCTTGAAGATGTGG 7710

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QY 1108 gaaagcaaatcgcagatgaaatgtaacaggttaccactaatatgtctgtgtgcaagagc 1167
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DB 7711 GATTTGAATATCAAAAAGTTGTAGAGGTTGGCTCTCCAGTTGTGTAGTAGCTGTG 7770
QY 1168 ttctcaatctaaagagacaaatagaagattggaataactgttctaaagatcgaatcat 1227
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DB 7771 TTCTGAAACGAAAAGMAMACACTAGATTCAAGGAAGTAGAAGCAAAAGTCTAAGTT 7830
QY 1228 tctcaacaatgtatccgtatgacagatgttcacgtgtgtgtgtgtgtgtgtgtgtgt 1287
   || || || || || || || || || || || || || || || || || || || || ||
DB 7831 CCCAGAGATTGGCAGCTTGGAAGAGACGATATCTAATTTGATTTCAGTTACAGATTT 7890
QY 1288 tgaacagcgaatcaaaaacatgtcttctgcatcttgaaatttccagaagacagtata 1347
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DB 7891 TACCACACTATCTTAAGCCCTGTTTCTCATTTTGGAGAGATTTTGCAGGAAGATGA 7950
QY 1348 ttccagtgaaagatttgatgatacatgatagtctgaggggtctc-----gaagttg 1401
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DB 7951 TTCTATCTTCAAAAATGACCAGTTGTGGGTACTGTGAAGGCTTGTACAAACAAACAG 8010
QY 1402 aaatgatgttgaagagagaggttgagaaggtgttgcaagagcttgcagatagatctag 1461
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DB 8011 AAAAAGCACAAGAGATACCGCACAAAGTTCTTGGACGATCTTATTTGATGGAATGTAG 8070
QY 1462 tctctgcagcaagagagatcagatgtaacaaaatagatcatgtlaagttcatcatc 1521
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DB 8071 TGATGGCATGAGAGAGAGACCTAAT--ACCAAGGTGAAGAGCTGCCGATTCATGATTT 8127
QY 1522 taatataagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1581
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RESULT 7
US-09-228-246-1
; Sequence 1, Application US/09228246
; Patent No. 6245510
; GENERAL INFORMATION:
; APPLICANT: Staskawicz, B. S. et al.
; TITLE OF INVENTION: PRF Protein and Nucleic Acid Sequences: Compositions
; FILE REFERENCE: 51700
; CURRENT APPLICATION NUMBER: US/09/228,246
; EARLIER FILING DATE: 1999-01-11
; EARLIER APPLICATION NUMBER: 08/680,327
; EARLIER FILING DATE: 1996-07-11
; EARLIER APPLICATION NUMBER: 08/310,912
; EARLIER FILING DATE: 1994-09-22
; EARLIER APPLICATION NUMBER: 08/227,360
; EARLIER FILING DATE: 1994-04-13
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 10968
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3879)..(8186)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (8300)..(9466)
; US-09-228-246-1

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Query Match      5.5%; Score 170; DB 4; Length 10968;
Best Local Similarity 50.6%; Pred. No. 5.2e-38;
Matches 547; Conservative 0; Mismatches 515; Indels 18; Gaps 5;

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DB 7120 CATCTTTTCAGCTTACTCAAGAGCAAGCAAAATGGAGGTTTTCAGATACAA 7179

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QY 568 ggaacagctgttagaagatcctgactagatcctctctggtggaacccaagatcccca 627  
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 QY 628 ttgtcggatgggagcataggttaaaacaaccttagaagaagaagttatcatatgaat 687  
 Db 7237 tctgtgcaagccagagattggcagaactacacagcaagaagatttaccatgatccag 7236  
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 QY 1522 taatatgagactgt 1581  
 Db 8128 tgtgtcaataattcgtcagtgaaagccaaacaaagagagatttcttctcacaata 8187

RESULT 8  
 US-08-310-912A-157  
 ; Sequence 157, Application US/08310912A  
 ; Patent No. 5981730

GENERAL INFORMATION:  
 APPLICANT: Ausubel, Frederick M.  
 APPLICANT: Staskawicz, Brian J.  
 APPLICANT: Brent, Andrew F.  
 APPLICANT: Dahlbeck, Douglas  
 APPLICANT: Katagiri, Fumiaki  
 APPLICANT: Kunkel, Barbara N.  
 APPLICANT: Mindrinos, Michael N.  
 APPLICANT: Yu, Guo-Liang  
 TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND DETECTION  
 NUMBER OF SEQUENCES: 208  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fish & Richardson P.C.  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02110-2904  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30B  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/310,912A  
 FILING DATE: September 22, 1994  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/227,360  
 FILING DATE: April 13, 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Lech, Karen F.  
 REGISTRATION NUMBER: 35,238  
 REFERENCE/DOCKET NUMBER: 00786/254001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 542-5070  
 TELEFAX: (617) 542-8906  
 TELEX: 100254  
 INFORMATION FOR SEQ ID NO: 157:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5134 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA  
 US-08-310-912A-157

Query Match 5.3%; Score 164.2; DB 2; Length 5134;  
 Best Local Similarity 50.3%; Pred. No. 1.5e-36;  
 Matches 544; Conservative 0; Mismatches 518; Indels 19; Gaps 5;

QY 508 caagttcaacaacagatatttgaagtgaaagaacataatgtgtgagctgagatgataa 567  
 Db 1136 CATCTTTTACCTTATCTACTCAAGAGCAAGCAAGCAATGAGGCTTTTCAGATACAA 1255  
 QY 568 ggaacagctgttagaagatcctgactagatcctctggtggaacccaagatcccca 627  
 Db 1256 TAGATGAATTAAGGATTAACACTGTGAGGATCACT--GAGCTTGATGTCACTCA 1312  
 QY 628 ttgtcggatgggagcataggttaaaacaaccttgcaagaagaagtttaccatgtatgat 687  
 Db 1313 TCGTTGGCATGCCAGGATGGCAAGACACACTAGCAAGAAAGATTTCAATGATCCAG 1372  
 QY 688 caattcctgcgttttgatgtatcgtcgtggtggtacacatactcacaagcacaanaa 747  
 Db 1373 AAGTCACTCTGCTTCGATGTCATGCTCATATGTGTGTGACTCAATATATATGATGA 1432  
 QY 748 aggaatttgcgtggtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 807  
 Db 1433 GAGAGTGTGTGCTCAACCAATTTGAATGATGTGCTTGAGCCTTCTGTATCGCAATGA 1491



Db 1967 taccacactcttaagcctgtttctctatttgagagattttgcagggaagata 2026  
Qy 1348 ttccagtgagaatttgatgatcatgtatgctgaggggttcctgaagttggaatg 1407  
Db 2027 ttcatgtaccacaaatagaccaggttggtagctgaagaagttgtacagcaacaag 2086  
Qy 1408 atttggaagagaggtt-----gagaagttgttcgaagctgttcgatagtcta 1460  
Db 2087 aaaaaagacaagaatgaccgcacaaagttcttgcagacatctatgtgaagaaatc 2146  
Qy 1461 gtccctgcagaagaagctgcagatggaacaaatagatcatgtaagttcatgat 1520  
Db 2147 gtagtgccatggaagagagactaatg---ccaagtgaaaaacgcccgcattcatg 2203  
Qy 1521 ctaatatagacctgtgcgtgagagaagttcaaaagggaagaacattttatcatgaacgc 1580  
Db 2204 ttgttcataaattctgcacatggaagcacaagaagagatttctctccacatcaat 2263  
Qy 1581 a 1581  
Db 2264 a 2264

## RESULT 10

PCT-US95-04589-157

Sequence 157, Application PC/TUS9504589

GENERAL INFORMATION:

APPLICANT: Ausubel, Frederick M.

APPLICANT: Staskawicz, Brian J.

APPLICANT: Brent, Andrew F.

APPLICANT: Dahlbeck, Douglas

APPLICANT: Katagiri, Fumitaki

APPLICANT: Kunkel, Barbara N.

APPLICANT: Mundrynos, Michael N.

APPLICANT: Yu, Guo-Liang

TITLE OF INVENTION: RPS2 GENE AND USES THEREOF

NUMBER OF SEQUENCES: 201

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish &amp; Richardson

STREET: 225 Franklin Street Suite 3100

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2904

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30B

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/04589

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/227,360

FILING DATE: 13-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 00786/230001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 100254

INFORMATION FOR SEQ. ID NO: 157:

SEQUENCE CHARACTERISTICS:

LENGTH: 5134 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

PCT-US95-04589-157

Query Match 5.3%; Score 164.2; DB 5; Length 5134;  
Best Local Similarity 50.3%; Pred. No. 1.5e-36;  
Matches 544; Conservative 0; Mismatches 518; Indels 19; Gaps 5;

Qy 508 caagttcaacaacagatatttgaaagttgaagaacatatggttgagcgtgatcaaa 567  
Db 1196 GATCTTTTTCAGCTTATCTCAAAAGAGCAACAGAAAGAGAGGTTTTCAGAGTACAA 1255  
Qy 568 ggaacagttgttaagaatctactagaagctactctgvggagcccaagatcccca 627  
Db 1256 TAGATGAATTTAAAGATTAACCTACTTGGAGATCAGCT---GAGCTTGAATGATCTCA 1312  
Qy 628 ttgctggagtgaggacataggtfaaaacacacttaagaagaagtttaccatgatga 687  
Db 1313 TCGTGGCATGCCAGGATTTGGCAAGACTACCTAGCAAGAAAGATTTACAAATGATCCAG 1372  
Qy 688 caattctatgcgcttctgattctatgctgcctggtcaccatctcaacagcaaca 747  
Db 1373 AAGTCACTCTCGCTTGCATGTCATGCTCATGATGTTGTGATCATTTATTCATGGA 1432  
Qy 748 aagaaatttgcctggcctctgcatccaacatcaaatgatatgaggttaagatga 807  
Db 1433 GAGAGTGTGCTCACCATTTTGAATGATGCTTGAAGCTTGCATGCCAATGAAGAAA- 1491  
Qy 808 ttggtgaagcagagctagcagacatgttacaagaagtttaagaagaagagttaa 867  
Db 1492 --GAGATGGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATG 1549  
Qy 868 ttgctctgatatcatctgagttgtaagttggaatgagcgtgagagcagatgcttcaa 927  
Db 1550 TTCTCATTTGATGATGCTGGGATGATTAAGTGTGGCAATCATGATGATGATGATG 1606  
Qy 928 ctgaagacaatgagagagtcgaatactgttgcacccglaatgatgaagttgctgt 987  
Db 1607 GTGATGTTCAAAATGAGAGATGATGATGATGATGATGATGATGATGATGATGATG 1666  
Qy 988 atgctgtgtgagaaatttctcttgvgatgagcttcaagatcaagaatgagaatgga 1047  
Db 1667 ATGTCAAAATGTAAGAGATGATGATGATGATGATGATGATGATGATGATGATG 1726  
Qy 1048 gtctttcaaaagtgacatttcaagtgaaagattacatcatgagttgagactgtg 1107  
Db 1727 CATTATTACGAAGAAGATGCTTTTCAAGAGAGAGCTTCCACCTGAACCTGAAGATG 1786  
Qy 1108 gaaagcaaatcgagatgaaatgttcaacggttaccactaactatgtcgtgttgagggc 1167  
Db 1787 GATTGAAATATCAAAAAGTTGTAGAGGTTGCTCTCAGTTGTGTAGTACTGCTG 1846  
Qy 1168 ttctcaaatcaaaagagacataagaattggaacatgttgcctaaagatgtaagtc 1227  
Db 1847 TTCTGAACACGAAAGAAAGACACTGATGATGATGATGATGATGATGATGATGAT 1906  
Qy 1228 tctgcacaatgtacctgaaagatggttcaacggtgtgtgtgtgtgtgtgtgtgt 1287  
Db 1907 CCAAGAGAGATTTGGCAGCTTGGAGAGAGCATATTTAATTTGGATTTAGTTACAA 1966  
Qy 1288 tgaacagcactcaaaaacatgttcttgcatttcggaattttccagaagacagtgata 1347  
Db 1967 TACCACTATTCATTAAACCTTTGTTTCTGATTTTGGAGATTTTTCAGAGAAAGATA 2026  
Qy 1348 ttccagtgagaatgtatgatcatgtatgctgaggggttccctgaagttggaatg 1407  
Db 2027 TTCAATGACTCAAAATGACCAAGTTGGGGTGAAGAGTTTGTCAAGCAAAACAGC 2086  
Qy 1408 atttggaagagaggtt-----gagaagttgttcgaagctgttcgatagtcta 1460  
Db 2087 AAAAAAGACAAGAGATACCCGCAAGGTTTCTTGAACATCTTATTTGGAGAAATCTG 2146  
Qy 1461 gtccctgcagaagaagtcgagatggaacaaatagatcatgtaagttcatgat 1520  
Db 2147 GTGATGCCATGAGAGAGAGACTAATG---CCAAGGTGAAGAAAGTCCCGCATTCATGAT 2203



```

Patent No. 6114605
GENERAL INFORMATION:
APPLICANT: Williamson, Valerie M.
APPLICANT: Kaloshian, Isouhli
APPLICANT: Yaghoobi, Jafar
APPLICANT: Bodeau, John
APPLICANT: Milligan, Stephen
TITLE OF INVENTION: Procedures and Materials for Conferring
Pest Resistance in Plants
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/947,823
FILING DATE: 09-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/18802
FILING DATE: 09-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,191
FILING DATE: 10-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-070210US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 51952 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-947-823-1

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Query Match 4.88; Score 149.2; DB 3; Length 51952;
Best Local Similarity 49.58; Pred. No. 9.9e-32;
Matches 512; Conservative 0; Mismatches 498; Indels 24; Gaps 4;

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QY 541 acaatatggttgacgtgatcatcaagaagaacagttgtagaagatcgtagaagct 600
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DB 46729 ATAAATAACGTGATGTTTGGAGGAAACAACTTGATTAAGAAGCTCACCACTG 46788
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 601 actctgggaacccaagatcccgatgtcggagatggagagcatagtaaaacct 660
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 46789 GATCGGCGAGATCTAGATCATCTTTTCGATCCTGCTGCGGTTCAAGTAAACTACTT 46848
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 661 tagcaaaagagtttaaatgaatcaatctcaatctttagtttagtgcctgg 720
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DB 46849 TGGCATCAAAAGTATACATAGTAAGTCAAGTTTCAAGCCGTTTCACTTCGTGATGCT 46908
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QY 721 ctaccatctcaacagcacacaacaaagaattgtctgggaccttgatcattccacaa 780
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DB 46909 GCACGGCTGCACCAAGAGTGTGAGAGAGTGTGAATAACATTTTCAAGTCAAGTTA 46968
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QY 781 tcaaatgtagatgacagggtagatgattgtagaagcagagctagcaacatgttaacaga 840
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 46969 GTGACTCAGAT-----TCAAAATTGAGTGAATATTGATGCTGTGATTAATTAACGGA 47022
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QY 841 aaagttaaagaagaagagtagtaattgtcttgatgatcatctggagttgtagatgt 900
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DB 47023 AACAACTGTTTGGAAAAGAGATCTTATTTGCTTAGATGAGCTGGGATFCTACTACAT 47082
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 901 gggatggcgtgagacagatgtcttccaactggaacaatgacagagatgacatgttga 960
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DB 47083 GGGATGAGTTTAAACAAGACTTTTC---CTGAATCTAAGAAAGAAAGTATGATTTTGA 47139
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QY 961 ctaccgtaatgtagatgtagctgttatgctgtgtgtagaagaattcttctggagaga 1020
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 47140 CAATCGGGAAGAAAGAGTGGCTTGCATGGAAAGCTGAACACTGATCTCTTGACTTC 47199
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1021 gcttcagatcaagaatgagagttggagctcttccaagaagcgacattccaagtgaag 1080
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 47200 GATTGCTAAGACCAAGATCAAGTTTGGGACCTATTAGAACAAAAGGCAATTGGGAATGGA 47259
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1081 cattaacatgagttcagagctgttggaagaacaatgcagatgagatgtagcgggttac 1140
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 47260 GTTGCCCTGATGAACTATTAGATGTCGTAAGAAATFAGCCGAAATTTGTAAGGGCTTC 47319
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1141 cactaacatgtcgtgtgttgacaggtcttccaactcaaaaagagacaatagagattga 1200
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 47320 CTTTGGTGGCTGATCTGATTCCTGAGTCATTCTGGAGGGAAGAAAGAGATGTGT 47379
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1201 aaactgttctaaagatgtaagtcacatcgtcacaacatgatcctgatgaacgatgttac 1260
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 47380 GGCCTTGAAGTTCAAAAGTATGATTTGAAGTTCTTTATTTTGAACAGTGAAGTGAATGA 47439
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QY 1261 gtgtgcttggttgagttagatcagatcaacttgacaagcagatcctaaacatgtcttcgact 1320
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DB 47440 AAGTTATGAAATTAAGTTATGATACCATTTTACACATCACTCAAGCAAGCTTGCTGTATTT 47499
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QY 1321 tcggaattttccagaagaacagatgatcctcagatgaagaatttgatgatcatgagcag 1380
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DB 47500 TTGCAAGTTTCCGAAAGCACTTCATTGACAAATTAAGATGATTTATTTTCGGTG 47559
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QY 1381 ctgaggggttctct-----gaagtggaaaatgatttggaagagagttgagaagtgct 1434
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DB 47560 CTGAAGAGATTTGTGGGAAAGACGAGATGACAGATGAGAGAAAGTGAAGATTTATA 47619
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QY 1435 tgcgaagctgtcgtatgtagtctagtcctcgttcgaagaagaagatcgagatgtaacaa 1494
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 47620 TGGATGATTTAATTACAGTAGCTGTGAATTTGTTAAATGAGATGATGATGATGCA 47679
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1495 aaattagatcatgtaagttatgatcctaataatagactgtgctgtagaagaagttcaaa 1554
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 47680 A-----TTTCCAAATTCATGATCTTGATGATGACTTTTGTGATTAAGAAAGCAAGA 47730
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1555 gggagaacatttt 1568
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 47731 AGGAAAATTTGTTT 47744
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```

```

RESULT 13
US-08-947-823-4
Sequence 4, Application US/08947823
Patent No. 6114605
GENERAL INFORMATION:
APPLICANT: Williamson, Valerie M.
APPLICANT: Kaloshian, Isouhli
APPLICANT: Yaghoobi, Jafar
APPLICANT: Bodeau, John
APPLICANT: Milligan, Stephen
TITLE OF INVENTION: Procedures and Materials for Conferring
Pest Resistance in Plants
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/947,823
FILING DATE: 09-OCT-1997
CLASSIFICATION: 800
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/18802
FILING DATE: 09-OCT-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/028,191
FILING DATE: 10-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-07021005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ. ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3982 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 87..3860
OTHER INFORMATION: /note="Copy 2 cDNA for M1 nematode
OTHER INFORMATION: resistance gene of tomato"
US-08-947-823-4

```

```

Query Match          4.8%; Score 147.6; DB 3; Length 3982;
Best Local Similarity 49.4%; Pred. No. 6,9e-32;
Matches 511; Conservative 0; Mismatches 499; Indels 24; Gaps 4;

```

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QY 541 acaatgtgttgacgtgatgatcaagaagaacagttgttagaagatctgactagaagct 600
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1642 ATTAATAATATGTAGCTTTTGAGAGAGAGCAAACTTGATTAAGTCAACCACTG 1701
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 601 actctggagaccacaagatcccgatctgctggagatgagcataggaataaacacct 660
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1702 GACCCGCAAGATTAGATGTCATTTCCATCAACCGGTATGCCGGTTGAGGTAAGTACT 1761
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 661 tagcaaaagaagttacatgatgatcaatctatccgcttctgactgctgctgctgct 720
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1762 TGGCATATCAAAAGATATCAATGATTAAGTCTAGACATTTTGACCTTCGTCATGGT 1821
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 721 ctaccatctcaacagcacaacaaaagaatttgcctggcctctgcacatccacaa 780
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1822 GCACGGTTCATCAAGATATGACGACAAAGTTGTTGATATCAATTTTCAGTCAAGTTA 1881
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 781 tcaaaatgatgacagaggttaagatgattggaagcagcagctagcagcatgttaccaga 840
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1882 GTGGCTCAAT-----TCAAATTTGAGTGAGAAATTTGATGTGCTGATTAATTCGGA 1935
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 841 aaagttaaagaagaagagttacttaattgtcttgatgatatctggaagttgtgaagtt 900
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1936 AACCACTGTTTGGAAAGAGTATCTTATGCTTAGATGATGTCGAGTACTACTACAT 1995
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 901 gggatggcgttgagagatgctcttccacatgagacatgacagggagtcgaatactgttga 960
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1996 TGGATGATGTCACAAAGACCTTTTC---CTGAAGCTTAAGAAAGAGTATGATTAATTTTGA 2052
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 961 ctaccgtaagtgtgtagctgtttagctgctgctgctgctgctgctgctgctgctgctg 1020
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2053 CAACCTGAGAAAGAGAGTGGCTTTGATGAGAAAGCTGACACTGATCTCTTGACCTTC 2112
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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QY 1021 gctcatgcatcaagatgaggttgagctcttccaaagtgcagcatcttccaagtgaag 1080
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DB 2113 GATTGTATAGACAGATGAAGTGGGAACTTTAGATTAAGAGACATTTGATATGAGA 2172
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1081 cattacatatgattctgagactgttgaaagcaaatcgacagatgaaatgcaaggttac 1140
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2173 GTTCCCTGATGAACATTTAGATGTGCTTAAGAAAGTAAAGCGAAATTTGTAAGGGCTTC 2232
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1141 cactaatattgtctgttgctgagcgttctcacaatctaaagaagacatgaaattgga 1200
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2233 CTTTGTCGCTGATCTATGCTGAGTCAATGCTGAGAGGAGAAAGAGAGTGTGT 2292
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1201 aaactgtctaaagatgacatcgtcgcacaaatgcatctgacatgacagatgtccac 1260
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2293 GCGTTGAAGTTCAAGATTTAGTGTCTTTATTTTGAACAGTGAAGTGAAGTGA 2352
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1261 gtgtgcttggttgatgacatcacttgcacaaagcagctcaaaacatgtcttcact 1320
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2353 AGTTATAGATTAAGTTAGTACCATTTACCATCATCATCAAGCCATGCTTGTCTCACT 2412
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1321 tcggaatttccagaagacagatgatatccagtgaaagatttgatgacatgagtg 1380
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2413 TTGCACTTGGCCGAGAGACACTCTTTGACAAATCTATTTGTTTACGTTTATTTGGCTG 2472
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QY 1381 ctgaggggttctc-----gaagtgtgaaatgatttgaaagagaggttgagaagttc 1434
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2473 CTGAGAGATTTTGGAAGAACGAGATGAAGGATATAGAAGAGTGTGAAGTTATA 2532
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1435 tgcagaagctgtcgatagatgctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 1494
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2533 TGGATGATTTAAATTTCCAGTAGCTTGCTTAATTTGTTCAATGAGATAGTGAATACTGA 2592
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1495 aaattgatcatgtaaggtcatgataatataatgacccgtgctgagaaagttcaca 1554
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2593 A-----TTTCAATTCATGATCTTGTGATGATCTTTGTTGATTAAGCAAGAA 2643
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1555 gggagaacatttt 1568
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2644 AGCAAAATTTGTTT 2657
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 14
US-08-930-996A-3
Sequence 3, Application US/08930996A
Patent No. 6100449
GENERAL INFORMATION:
APPLICANT: FUDER, Robert
APPLICANT: ESHED, Yuval
APPLICANT: ORI, Naomi
APPLICANT: PARAN, Ilan
APPLICANT: ZAMIR, Daniel
TITLE OF INVENTION: A GENE FAMILY FROM THE 12 FUSARIUM RESISTANCE
TITLE OF INVENTION: LOCUS OF TOMATO AND USE THEREOF FOR TRANSFORMATION AND
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,996A
FILING DATE: 09-DEC-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05272
FILING DATE: 15-APR-1996

```

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: II 113,373  
FILING DATE: 13-APR-1995  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4465 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 204..3923  
US-08-930-996A-3

Query Match 2.7%; Score 83.6; DB 3; Length 4465;  
Best Local Similarity 47.6%; Pred. No. 1,1e-13;  
Matches 393; Conservative 0; Mismatches 409; Indels 24; Gaps 4;

QY 610 aaccacaagtcacccgattgctggatggagcagataggaataaacacacttagcaaaag 669  
DB 781 ATCTGACAGCGTTCATGCTTGAATGGCTGGGCAAGACACACTTGGCTAAAG 840  
QY 670 aattacaatgataatcattctatgcccgttttgatgctcatgctgggtacacat 729  
DB 841 CCGTATACATGATGAGAGTGTAAAGACCATTTGATTTGAAGCTTGGTTGTGTT 900  
QY 730 ctcaacagcacacaagaatttgcgtggcccttcgcatccacaatacaatgg 789  
DB 901 CCGAGCGCTTATGCTTTCAGATATACAAAGGTTACTTCAAGAAATGGCTCAATG 960  
QY 790 atacaagggttaagatgattggtgaagcagactagcagacatgttacgaaagttaa 849  
DB 961 ACTTAGTTGATGACAACTTAATC-----AGCTACAAAGTCAATTCAGAGAAAGATTAA 1014  
QY 850 aaggaagaggttacttaattctggtatgatacttgagtt-----tggaagtgagg 903  
DB 1015 AGGAAAGAGAGTTCTTATGCTGTGATGATGTGGAATGACACTACACAGAGTGG 1074  
QY 904 atgagcgtgaagcagctctccaaactgaacaatcagaggagtcgatactgtgacta 963  
DB 1075 ATGATTTGAGAAATGTTTTGTA---CAAGAGATATAGGAAGTAATATCTGTGACA 1131  
QY 964 cccgttaatgataagtagctgtgtatgctggtgtagaagatttcttcgcgtagagct 1023  
DB 1132 CAGGCAAGACAGCTGTGCTTATGATGATGCGAAATGACAAATAGCATGGCGCAATTGT 1191  
QY 1024 tcatgatacagatgagtgatgcttccaaatgtagcagcatttcaagtgaaagcat 1083  
DB 1192 CTACCCGAAGCTCTGCTCTTATTTCAAGACATGCAATTTGAAMACATGGATCTATGG 1251  
QY 1084 taccataatgagtcgagactgtgaaagcaaatcagacatgaatgacaggtgtacac 1143  
DB 1252 GACATTTGGAAGCTTGAAGAGGTGGAAGACAAATTCAGCTAATGCAAGAGATGGCCT 1311  
QY 1144 taactattgctggtgtgagaggtcttcaaatcaaaaggaacaatagaagattgga 1203  
DB 1312 TAGCTTGAAGAGCGCTGTGCGCATGTTAGCTCCAAATGAGAGTGAAGAGTGAAT 1371  
QY 1204 ctgttgtaagatgtaagtaattgtaacaatgtagtccatgataagcagatgttcaagt 1263  
DB 1372 GTATTTGAGAAAGTGA---TATGGAGCTGCGAGACAAATGACATATTACAG 1422  
QY 1264 tgcctggtgtgagttacatcactgtgacaagcagatcaaaacatgcttcatgactcg 1323  
DB 1423 CGTTAATGTTGAGCTACAAATGATCTTCTGCACATTTAAAGCCATGCTTTCTTTGTG 1482  
QY 1324 gaattttcagaagacagatgataatccagtgaaagattgtatgatacagtagtgctg 1383  
DB 1483 CAATATTTCTTAAAGATTATTCATTTAGGAAGAAACAGTTATTCATCTATGATGCCA 1542  
QY 1384 aggggttcctcgaagcttggaataatgatttgaaagagaggttgagaa 1429

DB 1543 ATGCTTGTACCTGTGGAAGATGAATATTCAGATTAGGCA 1588

RESULT 15  
US-08-232-463-14/C  
Sequence 14, Application US/08232463  
Patent No. 5670367  
GENERAL INFORMATION:  
APPLICANT: DORNER, F.  
APPLICANT: SCHEIFLINGER, F.  
APPLICANT: FALKNER, F. G.  
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,463  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/935,313  
FILING DATE:  
APPLICATION NUMBER: EP 91 114 300.6  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)836-9300  
TELEFAX: (703)836-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7218 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: pTZ9pC-F15  
US-08-232-463-14

Query Match 2.3%; Score 72.6; DB 1; Length 7218;  
Best Local Similarity 4.6%; Pred. No. 1,9e-10;  
Matches 18; Conservative 232; Mismatches 141; Indels 0; Gaps 0;

QY 208 aaaaagttagtccctggaaglatgttcaagaacttgagaanaaacaatgttttggg 267  
DB 1465 AAGTATTAAGATGAAGAAATTTGTACRRRRRRRRRRRRRRRRRRRRRRRRRR 1406  
QY 268 aaatgaggaatttgaagtagagtaagagaagttgcaagtcgctgctgtaatacaatc 327  
DB 1405 RRR 1346  
QY 328 aacgagactacaggaacttactgagagaataaagccagaaaaaagcgctc 387  
DB 1345 RRR 1286  
QY 388 gaagtttcgcaagactgcaacaagtagcagagacatgatactggaagaagt 447  
DB 1285 RRR 1226





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 12, 2002, 11:30:22 ; Search time 66.67 Seconds  
(without alignments)  
1507.751 Million cell updates/sec

Title: US-09-864-680-3

Perfect score: 4712  
Sequence: 1 MAHASVAMTIRTESLTFN.....PVDVRISNPLKESDSEER 905

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: A\_Geneseq\_032802.\*  
2: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.\*  
3: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.\*  
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19: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.\*  
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23: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4712	100.0	905	AAE05409	Pepper Bs2 protein
2	4712	100.0	905	AAE05409	Pepper Bs2 amino a
3	1242.5	26.4	912	AA144818	Potato Gpa2 resist
4	1242.5	26.4	938	AA144818	Protein encoded by
5	1234.5	26.2	937	AA152152	Potato resistance
6	1234.5	26.1	937	AAU02143	Rx 25, modified re
7	1231.5	26.1	937	AAU02145	Rx 72, modified re
8	1230.5	26.1	937	AAU02148	Rx 7, modified res
9	1225.5	26.0	937	AAU02144	Rx 26, modified re
10	1221.5	25.9	937	AAU02146	Rx 39, modified re
11	1218.5	25.9	937	AAU02149	Rx 32, modified re

12	1215.5	25.8	937	AAU02147	Rx 193, modified r
13	980	20.8	1822	AAW48360	Tomato Prf protein
14	852.5	18.1	1255	AAW55974	Tomato pest resist
15	834.5	17.7	1206	AAW47080	Tomato MI resist
16	834.5	17.7	1206	AAW53583	Tomato MI resist
17	834.5	17.7	1207	AAW53582	Wild tomato Mi res
18	828.5	17.6	1257	AAW55975	Tomato pest resist
19	711.5	15.1	309	AAU02151	Plant resistance p
20	669	14.2	1266	AAW25157	Tomato immunity 2
21	669	14.2	1266	AAW07754	Amino acid sequenc
22	668	14.2	1240	AAW03665	IC-2 protein conf
23	605.5	12.9	953	AAW58854	Sorghum resistance
24	604.5	12.8	1220	AAW03664	IC-1 protein conf
25	554	11.8	901	AAW01966	A protein giving a
26	554	11.8	901	AAW01926	Rice probenazol re
27	553	11.7	901	AAW01925	An antidiasee gen
28	553	11.7	901	AAW01965	A protein giving a
29	553	11.7	901	AAW01925	Rice probenazol re
30	520	11.0	1205	AAW49434	Blast disease-resi
31	520	11.0	1251	AAW93135	Rice blast fungus-
32	503.5	10.7	1969	AAW72419	Rice bacterial lea
33	476	10.1	784	AAW64151	Lettuce resistance
34	451.5	9.6	1402	AAW64150	Lettuce resistance
35	447.5	9.5	1279	AAW39634	zea mays Rpg1-13 p
36	439.5	9.3	1294	AAW39633	zea mays Rpg1-2 pr
37	428.5	9.1	917	AAW80132	Rps2 disease resist
38	428.5	9.1	965	AAW83440	A.thaliana RPS2 po
39	428	9.1	342	AAW09957	Rice disease resist
40	410.5	8.7	928	AAW69308	Protein encoded by
41	408.5	8.7	928	AAW69307	Protein encoded by
42	376.5	8.0	1292	AAW39631	zea mays Rpi-D pro
43	376.5	8.0	1292	AAW39632	zea mays Rpi-D pro
44	375	8.0	396	AAU02152	Plant resistance p
45	366	7.8	1074	AAW64186	Lettuce resistance

## ALIGNMENTS

RESULT 1	AAE05409	standard; Protein; 905 AA.
XX	AAE05409;	
AC	24-SEP-2001	(first entry)
DT	Pepper Bs2 protein.	
XX		
DE	Bs2; pepper; resistance gene; plant pathogen; virulence gene;	
XX	bacterial spot disease; Xanthomonas campestris pv. vesicatoria;	
KW	AVBBS2; hypersensitive response; transgenic plant; tomato; tobacco;	
KW	rice; corn; wheat.	
XX		
OS	Capsicum annuum.	
XX		
PN	US6262343-B1.	
PD	17-JUL-2001.	
XX		
PF	23-JUL-1999;	99US-0360186.
XX		
PR	23-JUL-1998;	98US-0093957.
XX		
PA	(RESC ) UNIV CALIFORNIA.	
XX		
PI	Slaskawicz BJ, Dahlbeck D, Tai TH;	
XX		
DR	WPI: 2001-450496/48.	
XX	N-PSDB: AAD10203, AAD10204.	
PT	Nucleic acid molecules encoding Bs2 protein, useful for producing	
PT	transgenic plants having resistance to the plant pathogen Xanthomonas	

PR campestris -  
 XX Claim 1; Column 55-60; 37pp; English.  
 XX The present sequence is Bs2 protein from pepper. The Bs2 gene is shown  
 CC to confer resistance to plant pathogen from pepper. The Bs2 gene is shown  
 CC Xanthomonas campestris pv. vesicatoria which causes bacterial spot  
 CC disease. The Bs2 protein has Bs2 biological activity, i.e., when  
 CC co-expressed in a plant with a X. campestris AvrBs2 gene product,  
 CC it produces a localised hypersensitive response. The protein  
 CC includes a nucleotide binding motif and leucine rich repeats of the  
 CC type found in other plant resistance genes. The Bs2 nucleic acid  
 CC molecule is useful for producing transgenic plants such as pepper,  
 CC tomato, tobacco, broccoli, cauliflower, cabbage, cowpea, grape, canola,  
 CC bean, soybean, rice, corn, wheat, barley, citrus, cotton, cassava and  
 CC walnut, that are resistant to plant pathogen Xanthomonas campestris.  
 CC The transgenic plants produced using Bs2 molecule develop a  
 CC hypersensitive response to the pathogen at the site of inoculation and  
 CC show an enhanced resistance to systemic infection. The Bs2 nucleic acid  
 CC molecule is also useful as polymerase chain reaction (PCR) primers for  
 CC amplifying portions of Bs2 nucleic acid molecule, as sequencing primers  
 CC to verify the authenticity of an amplified molecule, and as  
 CC hybridisation probes.  
 XX  
 SQ Sequence 905 AA;  
 Query Match 100.0%; Score 4712; DB 22; Length 905;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 905; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAHASVASLMRTIESLTFNSPMOSLSCHREELCALREKVSLEVFKNFEKNVGEEM 60  
 DB 1 mahasvaslmrtieslftfnspmgsiscdhrreelcalreksvlefvknteknnvfem 60  
 QY 61 TDFEVEVREVASAEYITQLRLTGTIVLGENKSQKKARRRRRSGLQVYAEEMHIKVEST 120  
 DB 61 tdfvevrevasaeyitqlrltgtivgenksqkkarrrrrsglqvyaemdhikvest 120  
 QY 121 KIDQKGVSKESLVHDFSSSTNDILKKNMNGRDOOROLDLFRFSYSGEPKVPITV 180  
 DB 121 kidqkgvskeslvhdfssstndilvkknmvgrrdqtkqllledlfrfsysgepkvpitv 180  
 QY 121 kidqkgvskeslvhdfssstndilvkknmvgrrdqtkqllledlfrfsysgepkvpitv 180  
 QY 181 GMSGIGTTLAKVEYNDESILCRPDVHAMATISQOHKKRELLGLLHSTIKMDRVMKIG 240  
 DB 181 gmsgigtltlakevyndesilcrfdvhamatisqghnkellglhlstikmdrvmig 240  
 QY 241 EAEIADMLQSLKRRRLIYLDIWSCEWMDGVRRCPTEDNAGSRILLTTRNDEVACYA 300  
 DB 241 eaeladmlqslkrrrliylldiwscewmdgvrircptednagsrillltrndevacya 300  
 QY 301 GVENFSLRMSFMDDESMSLEKSAFSEALPYEFETVGOIADEGHPLTIYVAVGLL 360  
 DB 301 gvenfslrmsfmdesmslefsaafsealpyefetvgyqiaecnglptliyavagl 360  
 QY 361 KSKRTIEDMTKAVAKVSFTYNDPDERCSRVLGSLYDHLTSDLTCLLHFGIPEDSDIP 420  
 DB 361 kskrtiedmtkavakvsftyndpdercsrvglsydhlsdltcllhfgifpedsdip 420  
 QY 421 VKNIMRSMWABGLKLENDLEGEVEKCLQELVRCILVSKRSKDGKIKNSCKVHLLIYD 480  
 DB 421 vknimrsmwabglkklendlegeveklqelvrcilvskrsdgtkiknsckvhdliyd 480  
 QY 481 LCYREVORENFIINDIVLVSYDECSYLCMYKQKPRKRYTGOEINCPGLVYALLTPV 540  
 DB 481 lcyrevorenfiindivlvsvsydecsylcmymkqprkrytgoeinpcplvyalltpv 540  
 QY 541 NRQLRHDNNNLKRTSHVSFHLPEPLLYVLKSEVHFLLKLVLELHRQIDGPREILS 600  
 DB 541 nrqlrdhnnnlkrtshvsfhlpeplyvlksevhfllkvllelhrqidgpreils 600  
 QY 601 LILWRYLSLFSYGNFVPPETICRMNIQTITVQFRSDIILFBEIWEMLQRLHKLPRF 660  
 DB 601 lilwrylslfsygnfvppeticrlniqtitvqfrsdiilfbeiweamlqrlhklprf 660

DB 601 liwrylsifsygnfdvppeticrlwnlqtflvqfrfsdliifaeiweamlqrlhklprf 660  
 QY 661 YLPDPSGVKGRHLDPSNLQTTISYLSPPRCTKEVIGIQNVKKIGISGNDDVKSPRD 720  
 DB 661 ylpdpsgvkgrhldpsnlttisyyspprctkevignvkkigisgnddvksprf 720  
 QY 721 SGLPNNLVYLOQLLETLSISVDYSELPIVISSAKAPATLKKLERTYLSNSYLDIAE 780  
 DB 721 sglpnnlvylqllletlsisvdsyllpviissakafpatlkklerlylsyldiae 780  
 QY 781 LPNLEVLKMDACCCEGEMHPIVWGFNRKLKLLIYSLFKTWKAKANDPVLIERMTISC 840  
 DB 781 lpnlevlkmddaccgeemhpiwngfinrklilkyisflktwkatndhfpvlerimisc 840  
 QY 841 KNLKEIPREFADHITLQLEIRECPKLGESARIQKOEIDGNPNPVIRISNPLKESDS 900  
 DB 841 knlkeiprefadhtlqlleirecpklgesaariqkegedgnpnvdirisnplkesds 900  
 QY 901 DSEEH 905  
 DB 901 dseeh 905  
 RESULT 2  
 AAB72198  
 ID AAB72198 standard; Protein: 905 AA.  
 XX  
 AC AAB72198;  
 XX  
 DT 02-MAY-2001 (first entry)  
 XX  
 DE Pepper Bs2 amino acid sequence.  
 XX  
 KW Bs2; pepper; pathogen resistant; Xanthomonas campestris pv vesicatoria;  
 KW xcv; bacterial spot disease; transgenic plant; crop: fruit; flower.  
 OS Capsicum annum.  
 XX  
 PN WC200107635-A1.  
 XX  
 PD 01-FEB-2001.  
 XX  
 XX 23-DEC-1999; 99WC-US30891.  
 PF  
 PR 23-JUL-1999; 99US-0360186.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Staskawicz BJ, Dahlbeck D, Tai TH;  
 XX  
 DR WPL: 2001-168560/17.  
 DR N-PsDB: AAF63301, AAF63302, AAF63303.  
 XX  
 PT Novel Bs2 polypeptide from Capsicum annum for producing transgenic  
 PT plants having resistance to bacterial spot disease caused by  
 PS Xanthomonas campestris pv vesicatoria (Xcv) -  
 XX  
 PS Claim 1; Page 61-64; 72pp; English.  
 XX  
 CC This invention relates to the amino acid sequence of the Bs2 protein  
 CC isolated from Capsicum annum (pepper). The protein and DNA sequences of  
 CC Bs2 can be used to confer resistance to the plant pathogen Xanthomonas  
 CC campestris pv vesicatoria (Xcv) which causes bacterial spot disease. Bs2  
 CC DNA and protein sequences are useful for producing transgenic plants such  
 CC as pepper, tomato, tobacco, broccoli, cauliflower, cabbage, canola,  
 CC cowpea, grape, bean soybean, rice, corn, wheat, barley, citrus, cotton,  
 CC cassava and walnut, having resistance to X. campestris. The protein and  
 CC DNA molecule are also useful for producing transgenic alfalfa, flax,  
 CC sunflower, safflower, brassica, peanut, clover, lettuce, cucurbits,  
 CC potato, carrot, radish, pea, lentils, apples, pears, peaches, apricots,  
 CC carnations and roses having resistance to X. campestris. The present  
 CC sequence represents the Bs2 protein of the invention.



```

Db      48 hegltllelevelleayttedmvsdesrnyflarvngkrstramgiffvlegalecldstv 107
Oy      117 KESTKIODKGOVSKKE--SLVHDFSSSTNDILKVKNNMNGRDORQOLEDLTRSYSGEP 174
      108 kymatsdsmkdlkpqtsslv---slpendvegenlmvgrenefemmdqldarg-grel 163
Oy      175 KVIPIVGMGIGKTTTLAKREYNDSEILICRPDYHAMATISQOHNKKEILLGLHSTIKMD 234
      164 evasivmgigkltlaaklysdpylmsrfidrakatvsgyevrnvllgllsitsdepd 223
Oy      235 RKAMTEALADMLOKSLKRRKRLVLDIWSCEVWDVGRCPFTEDNAGSRILLTRND 294
      224 -----ygladqlqkhlgyrylrvldlwtteaaddiklcfpdcn-gsrilllttrnv 275
Oy      295 EVACVAGVNFSLRMSFMDODESMSLFKSAFSS--ALHYEPFTVVKOTADECHGLPRT 353
      276 evaeayassgkpphmrlmfdeswnllhkkllfkegssyspelenyglqalckgdlplai 335
Oy      354 VVAVGLL-KSKRTIEDMKTVAQVKSFTVNDPDERCSRYLGLSYDHLTKTCLLHFGI 412
      336 tliagllskstkltdewgvaenrvsvsldleakcmrlyalsyhlphlpcflyfai 395
Oy      413 FPEEDSDIPYKNNMRSMAGFLKE--NDLEGEVEKCLQELVDRCILVSKSRDGTQR 470
      396 faederylnkllvelwavegflneeegksleevaetclnelvdrlslshvnsfdg-etq 454
Oy      471 SKVHDLIYDLCVREYORENIFIMNDIYLDVSYPEC--SYLCMYKQOPKRYTGDEINC 528
      455 rcmgmndvtrelcleare--nmfavnlygksdqscagcmgsfksr----- 499
Oy      529 PYGLRYALLTPVNRQLRDHNNNL---KRTHSVFSFHLREPLYLVKSEVHFLLKYL 584
      500 -----srslhneeeelwcrnseahsiltlci---fkcvylelsflvrvl 542
Oy      585 ELRHQIDGFPREILSLIMRLYSL-----FSYGNFDPPELCRLMNQOT 629
      543 dglitcplfpgvslslhlylrylrfnprrlqyrgskeavpslidlplsisslcyqt 602
Oy      630 F-IVQFRFSDI-IIFAEIWEIMQLRHLKLPFYLPDCPSGSVDGRIHDFSNLOTSYL 687
      603 klylprfncypflrpseillmpqlrklomgwnyl---rshpeptenr-lvlsiqclnel 658
Oy      688 SPROCTKEVINGIQVKKVLGSGNKDYSKPRDSGLPNNLYVLDQLETLISLISVDS--- 744
      659 nprctgslflrlfplkkllevfyvkedfrnkd1---ydfrylqylekla-fstyssasa 714
Oy      745 -----LTPVIISAKAPAPATLKK 762
      715 cflkntaplgstgdpqlrfgmethlethsratapptdvrtflp---pdcfprqlks 770
Oy      763 LKLERT-YLSWSYLDIAELPNEVLKIMDACCGEEMHPIVMGFNRLKLLIKYSFLKF 821
      771 ltfsgdflfawkdlisvqklpklevlqshnafkygeewevveegfphlkfllfidslyrr 830
Oy      822 WKANDNPFVLEIRLMIRSCNKLKEPIEFADITHLQLELRECPKLGESARIOKEED 881
      831 wraasdhpylerlflscfryldspfdadltalidlfrcqsgvynsaklqgdqld 890
Oy      882 LGNNPVDV 889
      891 nysgsiev 898
Db

```

```

RESULT 4
AAV45004
ID AAV45004 standard; Protein; 938 AA.
XX
AC AAV45004;
XX
DT 23-MAY-2000 (first entry)
XX
DE Protein encoded by potato Gpa2 resistance gene.
XX

```

```

KW      Resistance: Gpa2; potato; phytopathogenic nematode; chromosome 12p;
KW      marker; IPW4c; 11LR; Potato Cyst Nematode; PCN; Globodera; nematocide;
KW      nematode resistance; Nucleotide Binding Site; NBS; detection; diagnosis;
KW      transgenic plant.
XX
OS      Solanum tuberosum.
XX
FH      Key
FH      Binding-site
FT      Location/Qualifiers
FT      172..178
FT      /label= "P-loop_motif
FT      /note= "Conserved motif within the Nucleotide Binding
FT      Site (NBS). This region is specifically claimed"
FT      329..334
FT      /note= "Conserved motif within the Nucleotide Binding
FT      Site (NBS). This region is specifically claimed"
FT
FT      Binding-site
FT      329..334
FT
FT      WO200006753-A1.
FT
FT      10-FEB-2000.
FT
FT      31-JUL-1998; 98WO-NL00445.
FT
FT      31-JUL-1998; 98WO-NL00445.
FT
FT      (CPRO-) CPRO-DLO CENT PLANTENVEREDELINGS REPROD.
FT      (UYMA-) LANDBOUMUNIVERSITEIT WAGENINGEN.
FT
FT      Van Der Vossen EAG, Van Der Voort JNAMR, Lankhorst RMK, Bakker J;
FT      Stiekema WJ;
FT      WPI: 2000-195310/17.
FT      N-PSDB: AAZ50652, AAZ50653.
FT
FT      Recombinant Gpa2 polynucleotide from potato, Solanum tuberosum, useful
FT      to confer resistance to phytopathic nematodes of the genus Globodera in
FT      transgenic plants, e.g. resistance to potato cyst nematodes in potatoes
FT
FT      Claim 2: Page 50-54; 96pp; English.
FT
FT      The present sequence is that of Gpa2 protein encoded by potato Gpa2
FT      resistance gene, that confers resistance to infection by phytopathogenic
FT      nematode of the Globodera genus. Gpa2 gene is mapped to short arm of
FT      chromosome 12 (12P), between the markers IPW4c and 11LR. This locus is
FT      associated with resistance to Potato Cyst Nematodes (PCN) like G. pallida
FT      and G. rostochiensis, that invade and damage the roots of Solanaceae. It
FT      has nematocidal activity. Recombinant DNA sequence comprising the Gpa2
FT      gene can be used to produce transgenic plants with increased resistance to
FT      nematodes. The polypeptides can also be used in nematocidal compositions
FT      and for detection and diagnosis of nematode infections.
FT
FT      Sequence 938 AA;
FT
FT      Query Match 26.4%; Score 1242.5; DB 21; Length 938;
FT      Best Local Similarity 34.9%; Pred. No. 1.6e-99;
FT      Matches 344; Conservative 147; Mismatches 341; Indels 153; Gaps 30;

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```

QY 235 RVKMGAEALADMLQSLKRRKRYLIYDDIMSCVWDGVRCPPTEDNAGRILLTTRND 294
DB 224 -----YGLAQGLQHLLKGRYLVVLDIWLTEAWDDKLCPCDCA--GSRILLITRRV 275
QY 295 EVACVAGVNFSLRMSFMDQDSWSLFLKSAFSS--ALPYEFETVQKQIADCHGLPLTI 353
DB 276 evaeayassgkprhmrlnmfcdeswnllhkkifeegsyepetenlqkqalckgqjplal 335
QY 354 VVVAGLL-KSKRTIEDKVAKDVKSFTVNDPDERCSRYLGISYDHLTSDLTCLLHFGI 412
DB 336 tlaagllsklslkldewqnaevsvsstdleakcmrylalsyhlphlhpclfyfai 395
QY 413 FPEDSDIPYKNLMRSMWAGFLKLE--NDLEGEVEKCLQELDRCLVLSKRSRQDCTKIR 470
DB 396 feedetiynkllvelkavagflneeegksieevaetclnelvdrslslhmsfdg-eqg 454
QY 471 SCKVHDLIYDLCEVQORENIFIMNDIVLDSYPEC--SYLCMYKMKOPFRVYTGDEINYC 528
DB 455 rcmghdvtrclclrear--nmnfvnrlrgksdqscagmqsfkar----- 499
QY 529 PGLVYALLTPVNRQLRDNNNL-----KRHSVFSFHLERLYLKSEVHFKLLKYL 584
DB 500 -----srslhneelwvcrnseahsiltlcl---fkcvlelslklvryl 542
QY 585 ELRHRQIDGPREIISLIWRYLSL-----FSYGNFDPPEICRLNNLQF 629
DB 543 dglgttcplfpgsvslhlyslrlnprlqgyrskavpsalldplslslcyqlt 602
QY 630 F-IVQFRSDI-IIFAEIEMELQLRHLKLPREFLPDPSGSDYKGRHLDPSNMQTISYL 687
DB 603 flklyhpfncypflrlpselltmpqlrklcmgwnyl---tshptent-r-lvklqglnel 658
QY 688 SRRCCKEYIMQVKKLGISGNKDDYKSFSDGSLPNNLVYIQOEIISLISVDYS---- 744
DB 659 nprycgslflrlfplnlkklvfgkedfrnkdL---ydftrylyglekla-fslysssa 714
QY 745 -----LLPVTISAKFPATLKK 762
DB 715 cflkntaplgstppdqlrlrmetlhetstraptldptfllp-----ppdcfipnlhs 770
QY 763 LKLEERT-VLWSYSLDIIEALPNLEVLKLDMDACCGEWHPIVGFNRLLKLLIKYSFLK 821
DB 771 lftsgdfllawkdlisvqklprlevlqishnatkegeweevqfphlflfidslyty 830
QY 822 WATANDNFYLERLMRSCKNKLKEPIERADITLQILRECPPLKLSAANIQOEQED 861
DB 831 wrasschfpylerlflsdcfyldsprdfadltlalldlftcqsavgsnakqldqld 890
QY 882 LGNNPVDVRI---SNPLKESDSDS 902
DB 891 nygssieskwsifgsvttddddd 915

```

RESULT 5  
AAV52152  
ID AAV52152 standard; protein; 937 AA.

```

XX AAV52152;
XX
XX 01-FEB-2000 (first entry)
XX
XX Potato resistance X protein sequence.
XX
XX Potato; Rx gene; resistance gene; potato virus X; PVX; transgenic plant;
XX broad spectrum extreme resistance; Narcissus mosaic virus; NMV; NVX; VNV;
XX Nandina virus X; Viola mosaic virus; Cymbidium mosaic virus; CYMV; PopMV;
XX Poplar mosaic virus; White clover mosaic virus; WCLMV; activate.
XX Solanum tuberosum.
XX
XX Key Location/Qualifiers
XX Region 168..180

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FT FT /note= "Kinase motif 1a"
FT Region 237..247
FT FT /note= "Kinase motif 2"
FT Region 265..273
FT FT /note= "Kinase motif 3a"
FT Region 330..342
FT FT /note= "R gene signature"
FT Region 386..396
FT FT /note= "R gene signature 2"
FT Region 458..467
FT FT /note= "R gene signature 3"
PN W09544490-A2.
PD 28-OCT-1999.
XX 16-APR-1999; 99MO-GB01182.
XX 16-APR-1998; 98GB-0008083.
XX
XX (PLAN-) PLANT BIOSCIENCE LTD.
PA Bendahmane A, Baulcombe DC, Kanyuka KV;
PI WPI; 1999-634006/54.
XX N-PSDB; AAZ37153, AAZ37154.
XX
XX New isolated plant virus resistance gene, used to produce transgenic
XX plants with resistance to virus infection
XX
XX Claim 5; Fig 1; 124pp; English.
XX
XX This is the amino acid sequence encoded by the potato Rx gene. The Rx
XX gene is a resistance gene which confers extreme resistance against
XX potato virus X (PVX). Sequence AAZ37154 is the Rx coding sequence free
XX from introns, while sequence AAZ37153 includes introns. The Rx gene can
XX be used to create a recombinant vector which encodes the Rx resistance
XX polypeptide AAV52152, this vector can be used to transform plant cells
XX to produce a transgenic plant with resistance to PVX. The Rx gene can be
XX used to engineer resistance traits, preferably broad spectrum extreme
XX resistance, into plants. The Rx gene can also be activated by non-PVX
XX viruses, e.g. Narcissus mosaic virus (NMV), Nandina virus X (NVX), Viola
XX mosaic virus (VMV), Cymbidium mosaic virus (CYMV), Poplar mosaic virus
XX (PopMV) and White clover mosaic virus (WCLMV). Rx can be used to offer
XX specific protection against this group. The Rx gene sequence can be used
XX to create antibodies specific for Rx. The antibodies can be used to
XX down-regulate Rx activity and also for the detection, identification or
XX isolation of Rx or homologues.
XX
XX Sequence 937 AA;
SQ

```

Query Match 26.2%; Score 1234.5; DB 20; Length 937;  
Best Local Similarity 35.1%; Pred. No. 8.2e-99;  
Matches 345; Conservative 144; Mismatches 343; Indels 151; Gaps 32;

```

QY 1 MAHASVASIMRTTESLTFNSPMQSLSCDREELCALREKVSLEYVKNFEKN-NVFE 59
DB 1 mayaaavtslmtl-----ngsmeltgdc---lqpfyeklksrall---ekscnimgd 47
QY 60 ---MTDFEVEVRVASAEYTIQLRITGLGENKKSQKKARRRFRROSLQOVEDMDHIW 116
DB 48 hegltlleveivayvaytcdmvsesrnlqalnleerstrameiffvlvaledcldst 107
QY 117 KESTKIQDKGQVSK--SLVHDFSSSTNDILKVNKNMGRDQROKOLEDLTRRSYSGEP 174
DB 108 kymatscdsmkdlkpgtsslv---slpehveqpenlmvgyrenefemuldqqlaryg- 163
QY 175 KYVPIYGMGIGKTTLAKKEYNDESLICRFVDYAMATISQOHHKKEILLGLSTIKMD 234
DB 164 evsvivgmglgkltclakysdpcmlstrlditakavsegyevrnvljgllslsdepd 223
QY 235 RVKMGAEALADMLQSLKRRKRYLIYDDIMSCVWDGVRCPPTEDNAGRILLTTRND 294

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Db 224 -----qldadrlqkhlkgrrrlyvldidivlteawddklcfpcocyn-gsrilllttrnv 275
Qy 295 EVACYAGVENFSLRMSFMDQDESWSLFKSAFSSSE-ALPYEEFYWGKOIADCHGLPLTI 353
Db 276 evaeyasgkpphhmrlnmfdeswnllhkkifekegsyspelenlgkqalckgslplai 335
Qy 354 VVVAAGLL-KSKRTIDMKTVAADVKSFTYNDPDECSRYLGISYHLSYDLTKCLLHGFI 412
Db 336 tvlagllskmgqrldewqrlgenvssvstdeaqcmrvtalsyhlpslhkpcflytai 395
Qy 413 FPEEDIDPVKNNLMRSMMAEGFLKLE--NDLGEVEKCLQELVDRCVLVSKRSRDTKIR 470
Db 396 ftedeqisvnelvelwpegflneeegksieevattcneidrsllfifmstfgt-le 454
Qy 471 SCKVHDLIYDLCCVREVQRENIFIMNDIVLDVSYPCSTYLCMKMPKRVGTDEINCPY 530
Db 455 scgmhdvtrelclearear--nmufvnl-----rgksdq-nscag 490
Qy 531 GLYRALLRPVNRQLRDHNNNL-----KRTHSVF--SPHLEPLYYVLKSEVYHFKILKY 583
Db 491 smqtrfks--srlllhveelawcrnseahslm1ggfecvtl-----elstkllytv 541
Qy 584 LELRRHROIQDEPRELLSLWLRYSL-----FSGNFDPYPERICRLMWLQ 628
Db 542 ldlgntwplfsgvylslhlrlyslrfpqlqygsakeavpslidlplalselcy1q 601
Qy 629 TPIVQ-RRRSDI-IFAEIWEIWMQLRHLKLPRTFLPCPSSSVKGRILDSNQTISY 686
Db 602 tkhlpfpyyplfllpsellmpqlrtcmgwnyl--rshpeetr-lv1knlqclnq 657
Qy 687 LSPRCCTFEVINGIONVKKLGISGNKDDYKSPRDSGLPNNLVYLOOLETSL----- 738
Db 658 lnprrctgsfflfnlklkqfygpedfrnsgdl---ydflylqleeltrlyypaa 714
Qy 739 -----ISVDYS-----LLPVIISAKAPATLKLKLER 767
Db 715 cflkntapsgstqdlrfqtelhkeidfgytappclllp---ppdatpqlklsitfgy 770
Qy 768 TY-LSMSVLDIAELPNEVLVKIMDACCGEHPIVMGFNKLKLLKYSLKFMRKATN 826
Db 771 efsvawkslsvgk1pkllevlllswaflgkeweevgefphk1fllddvy1rvtas 830
Qy 827 DNFVLERIMRSCNKLKEPIEFADITHLQLELRECPKLGESARIQKQEDLGNP 886
Db 831 dhfylevllrdrclnsldiprdaditcltalldidycqsvvnaskqdgldqnygss 890
Qy 887 VDVR1-----SNPLKESDSDS 902
Db 891 levhtrhlfipksvtlveddds 913

```

## RESULT 6

AAU02143 ID AAU02143 standard; Protein: 937 AA.

AAU02143; AC

AAU02143; DT 29-AUG-2001 (first entry)

DE Rx 25, modified resistance protein.

RX Rx; modified resistance; NBS; LRR; cell death; autoactivator;

KW nucleotide binding site; leucine rich repeat; pathogen resistance;

XX Solanum tuberosum.

XX OS Synthetic.

XX PN WO200129239-A2.

XX PD 26-APR-2001.

```

PF 12-OCT-2000; 2000WO-GB03930.
XX 15-OCT-1999; 99GB-0024483.
PR (PLAN-) PLANT BIOSCIENCE LTD.
PA Bendahmane A, Baulcombe DC;
XX WPI: 2001-290924/30.
DR N-PSDB; AAS03713.
XX
PT Modifying activation characteristics of plant resistance proteins to
PT produce autoactivator polypeptide capable of activation in absence of
PT elicitor, by introducing modifications in amino acid sequence of
PT protein.
PS Disclosure; Page 61-65; 77pp; English.
XX
CC The sequence represents the amino acid sequence of Rx 25, a modified
CC resistance autoactivator. Rx encodes an NBS-LRR polypeptide having a
CC nucleotide binding site (NBS), leucine rich repeat (LRR), and which
CC mediates cellular response leading to pathogen resistance and/or cell
CC death or dysfunction in response to an elicitor. The Rx was modified by
CC introducing modification to the amino acid sequence in absence of an
CC autoactivator polypeptide, capable of activation in absence of an
CC elicitor. Decoupling of resistance response from its natural elicitor is
CC useful for developing novel pathogen resistant plants. The modified
CC resistance proteins are useful for conferring resistance to non-natural
CC agents or stimuli and also for investigating resistance response pathways
CC and protein interactions e.g. with activators and repressors.
XX
SQ Sequence 937 AA;

```

Query Match 26 1%; Score 1231.5; DB 22; Length 937;  
 Best Local Similarity 35.0%; Fred. No. 1.5e-98;

Matches 344; Conservative 145; Mismatches 343; Indels 151; Gaps 32;

```

Qy 1 MAHASVASIMRTRESLTPNSPQSLCDHREELALREKVSLEVFYFNEKN-NVGE 59
Db 1 mayaavtskrtl-----hgsmltgc-----lqpfyeklsitrail---eksnlmgd 47
Qy 60 ---MTDFEVEVREVASAAEYTIQLRLTGTGLENKSQKKARRRRQSLQVADMDHIT 116
Db 48 heglfcllelvelevaytledmwsrnlvlagqleersamwelfvleglecidstev 107
Qy 117 KESTKIQDKGKQVSKK--SLVHDFSSSTNDILKAVNNWGRDQKOLLEDTFRYSGRP 174
Db 108 kqmatdsamkdklqptsllv--slpendveqpenlmvgtenelemldq1arg-grel 163
Qy 175 KVIPIVGMGIGKTTLAKENVYNDSEILCFRDVHAMATTISQUNKKEIILGLHSTIKMD 234
Db 164 evvsivgmgiqtktlackllysdpcimarfdrakatsvgeycvnnvllgllslsdepd 223
Qy 235 RVKMTIGEALDMLQSLKRRRYLIVLDIWSCEVWDGVRCEPTEBDNAGSILLTTRND 294
Db 224 -----qldadrlqkhlkgrrrlyvldidivlteawddklcfpcocyn-gsrilllttrnv 275
Qy 295 EVACYAGVENFSLRMSFMDQDESWSLFKSAFSSSE-ALPYEEFYWGKOIADCHGLPLTI 353
Db 276 evaeyasgkpphhmrlnmfdeswnllhkkifekegsyspelenlgkqalckgslplai 335
Qy 354 VVVAAGLL-KSKRTIDMKTVAADVKSFTYNDPDECSRYLGISYHLSYDLTKCLLHGFI 412
Db 336 tvlagllskmgqrldewqrlgenvssvstdeaqcmrvtalsyhlpslhkpcflytai 395
Qy 413 FPEEDIDPVKNNLMRSMMAEGFLKLE--NDLGEVEKCLQELVDRCVLVSKRSRDTKIR 470
Db 396 ftedeqisvnelvelwpegflneeegksieevattcneidrsllfifmstfgt-le 454
Qy 471 SCKVHDLIYDLCCVREVQRENIFIMNDIVLDVSYPCSTYLCMKMPKRVGTDEINCPY 530
Db 455 scgmhdvtrelclearear--nmufvnl-----rgksdq-nscag 490

```

[illegible]

RESULT:	7
AAU02145	
ID	AAU02145 standard; Protein; 937 AA.
XX	
AC	AAU02145;
XX	
DT	29-AUG-2001 (first entry)
XX	
DE	Rx 72, modified resistance protein.
XX	
KW	Rx: modified resistance; NBS; LRR; cell death; autoactivator; nucleotide binding site; leucine rich repeat; pathogen resistance; plant.
KW	
XX	
OS	Solanum tuberosum.
OS	synthetic.
XX	
PN	WO200129239-A2.
XX	
PD	26-APR-2001.
XX	
PF	12-OCT-2000; 2000MO-GB03930.
XX	
PR	15-OCT-1999; 99GB-0024483.
XX	
PA	(PLAN-) PLANT BIOSCIENCE LTD.
XX	
PI	Bendahmane A, Baulcombe DC;
XX	
DR	WPI: 2001-280924/30.
DR	N-PSDB; AAS03715.
XX	
PT	Modifying activation characteristics of plant resistance proteins to produce autoactivator polypeptide capable of activation in absence of elicitor, by introducing modifications in amino acid sequence of protein -
XX	
SS	Disclosure; Page 61-65; 77pp; English.

CC The sequence represents the amino acid sequence of Rx 72, a modified  
CC resistance autoactivator. Rx encodes an NBS-LRR polypeptide having a  
CC nucleotide binding site (NBS), leucine rich repeat (LRR), and which  
CC mediates cellular response leading to pathogen resistance and/or cell  
CC death or dysfunction in response to an elicitor. The Rx was modified by  
CC introducing modification to the amino acid sequence to produce an  
CC autoactivator polypeptide, capable of activation in absence of an  
CC elicitor. Decoupling of resistance response from its natural elicitor is  
CC useful for developing novel pathogen resistant plants. The modified  
CC resistance proteins are useful for conferring resistance to non-natural  
CC agents or stimuli and also for investigating resistance response pathways  
CC and protein interactions e.g. with activators and repressors.  
XX  
XX Sequence 937 AA;  
SQ

Query Match	26.1%	Score 1231.5	DB 22	Length 937
Best Local Similarity	34.9%	Pred. No. 1.5e-98		
Matches 343	Conservative 143	Mismatches 36	Indels 151	Gaps 31
OY	1 MAHASVASIMRITESLTFPNSQSIQCHREELCALREKVSLSLEVFNFEKN-NVPEE	59		
Db	1 mayaavtslmrl-----hgsmtelgdc---lqpfyeklsitrail---ekscingd	47		
OY	60 ---MTDFEVEYEVASAAEYTIQLRLTGTVLGENSEQKKARRRROSLQOYAEEDMHI	116		
Db	48 hegltlelevelveaytledmwsdesrnvlagnleersramwellfyleglecdistv	107		
OY	117 KSTYIKODKGRKVSNE--SLVHDFSSSTNDILAKVNNWGRDQKOLLIEDTRISGEP	174		
Db	108 kymtasdmkiklqtslvs---slpendveqpenlmvgreentemldqlary-grel	163		
OY	175 KVIPIVGMGLGKTTTLAKEVYNDESLICRFVDVNAATLSQCNKKEIILGLHSTIKMD	234		
Db	164 evslsvmgvgigkttlactklysdpcimserdtkratvsgcyevrnvlqllstsdgpd	223		
OY	235 RYKMTIGEAFLDMLOKSLKRRYTLVDDIMSCYEWGVRRCPEPDNNGSRILLTTRND	294		
Db	224 -----dqladrlqkhlkgyrrylvaviddlwtfeawddkiklcfpcygn-gsrilllttrnv	275		
OY	295 EVACYAGVENFSLRSPMDODESWSLFRKSAASSE-ALPYEPFYGKQIADCHLPLTI	353		
Db	276 evaegysagsgkprphmrlnmfideswlllkkkifeqsgsyfepenigkqialkcggllpai	335		
OY	354 VYVAGIL-KSKRTIEDMKTVAAVKSFPYTNDEPDRCSRYLGSYDHLTSDKTCYLHFGI	412		
Db	336 tvlagllakmggrldewgrlgenvsavstcpeaqcmvrlalsylhlpshlkpctfyfa	395		
OY	413 PFEDSDIYVKNLMRSMWAEGLKLE--NDLBEVAKCIQELVDRCLVLVSKRSRGCTAIR	470		
Db	396 fteveqisvnelvelwlpregflneeqgksleavattcnelldrelifhmfisfgrt-le	454		
OY	471 SCKVHDLIYDLCVREVORENIFIMNDIYLDVSYPCSLCYMKMPKFRWGTDEINCPY	530		
Db	455 scgmhdvtrclchrear--mmftrvyl-----rgsdsq-nscag	490		
OY	531 GLYRALLTPVNRQLRDHDNNNL-----KRTHSVF--SFHLPEPLYLKSEVYHFKLLV	583		
Db	491 smgrsfks--tsrtilfhvveelawcgrnseanslmlggfecvlt-----elstfklyrv	541		
OY	584 LELRRRQIDGPRELSTLIMLRYLSL-----FSYGNFVVPPEICLWMQ	628		
Db	542 ldlglntwplrfpsgyalslthlyrlsrlfnpclqgyqsgskaavpsalidipisisselyq	601		
OY	629 TFIYVQ-RFRSDI-IIFAEIIWLMQLRLHKLPRFLYLPDPCPSGSYVKGRRHDFSMLQTSY	686		
Db	602 tfklmlpfpsyyplfjselltmpqlrtclmgwyl-----fshptgrlrvlknlqclng	657		
OY	687 LSPRCCTKEVIMIGIONVKKLGISGKKDDXKSPRDSGLPNNLVLYQQLITSL-----	738		
Db	658 lnpfycgtsftrlfnlkkkqvgfyvpedfinsqdl---ydyftrlyqleeltrlyypaa	714		
OY	739 -----ISVQYS-----LLPVIISGAKAPATLKKLKER	767		

Db 715 cflktapsstqdbdlrfqteillkeidfgtaptlllp-----ppdaifpnllslftrg 770  
 Qy 768 rY-LSMSYDITAEIPNLEVLKMDACCGEHPIVGFNRKLLIKYSFLKFWKATN 826  
 Db 771 etsvawkdslstvgkpkhlevillswatfigkewevgeefhpkfildvdyityrass 830  
 Qy 827 DNEPVLERIMTSCNKLKEIPREFDHTLQLEIRECPPLGESAARIQKQEDLGNP 886  
 Db 831 dhfpylevrlidcrnlslprdfaditlaldidycqgvsvnsakqldqdnys 890  
 Qy 887 VDVRI-----SNPKESDSDS 902  
 Db 891 levhtrhlfipksvtvdedds 913

RESULT 8  
 AAU02148  
 ID AAU02148 standard; Protein; 937 AA.  
 AC AAU02148;  
 DT 29-AUG-2001 (first entry)  
 DE Rx 7, modified resistance protein.  
 KW Rx; modified resistance; NBS; LRR; cell death; autoactivator;  
 KW nucleotide binding site; leucine rich repeat; pathogen resistance;  
 KW plant.  
 OS Unidentified.  
 FH Key Location/Qualifiers  
 FT Misc-difference 162 /note= "Encoded by gac"  
 FT Misc-difference 177 /note= "Encoded by cca"  
 FT Misc-difference 178 /note= "Encoded by cca"  
 FT Misc-difference 218 /note= "Encoded by cct"  
 FT Misc-difference 221 /note= "Encoded by cca"  
 FT Misc-difference 430 /note= "Encoded by gac"  
 FT Misc-difference 585 /note= "Encoded by cca"  
 FT Misc-difference 585 /note= "Encoded by gac"  
 FT Region 1..786 /note= "Only amino acids 1-786 are encoded by the  
 cDNA sequence shown in the specification  
 and given in AAS03718"  
 PN WO200129239-A2.  
 PD 26-APR-2001.  
 PF 12-OCT-2000; 2000MO-GB03930.  
 PR 15-OCT-1999; 99GB-0024483.  
 PA (PLAN-) PLANT BIOSCIENCE LTD.  
 PI Bendahmane A, Baulcombe DC;  
 DR WPI: 2001-290924/30.  
 DR N-PSDB; AAS03718.  
 XX Modifying activation characteristics of plant resistance proteins to  
 PT produce autoactivator polypeptide capable of activation in absence of  
 PT elicitor, by introducing modifications in amino acid sequence of  
 PT protein -  
 PS Disclosure: Page 61-65; 77pp; English.

XX The sequence represents the amino acid sequence of Rx 7, a modified  
 CC resistance autoactivator. Rx encodes an NBS-LRR polypeptide having a  
 CC nucleotide binding site (NBS), leucine rich repeat (LRR), and which  
 CC mediates cellular response leading to pathogen resistance and/or cell  
 CC death or dysfunction in response to an elicitor. The Rx was modified by  
 CC introducing modification to the amino acid sequence to produce an  
 CC autoactivator polypeptide, capable of activation in absence of an  
 CC elicitor. Decoupling of resistance response from its natural elicitor is  
 CC useful for developing novel pathogen resistant plants. The modified  
 CC resistance proteins are useful for conferring resistance to non-natural  
 CC agents or stimuli and also for investigating resistance response pathways  
 CC and protein interactions e.g. with activators and repressors.  
 XX Sequence 937 AA:  
 SQ  
 Query Match 26.1%; Score 1230.5; DB 22; Length 937;  
 Best Local Similarity 35.1%; Pred. No. 1.8e-98;  
 Matches 345; Conservative 145; Mismatches 342; Indels 151; Gaps 32;  
 Qy 1 MAHASVASLMRTIESLTFNSPMQSLSCDRELCALREYVSLFVFNFEKN-NVPE 59  
 Db 1 mayaaavslmrtl-----hpsmeltgcyd---lqpfyexlkslraill--exsclmgd 47  
 Qy 60 ---MTDFEVEYREYASAEYTIQLRLTGVLGENKSQKKARRRFRQSLQOVVEDMDHW 116  
 Db 48 hegtlllelevelveaytiedmvsesrnfiaqlnestramwelfvlegalecdstcv 107  
 Qy 117 KESTIQDKGKOVSE--SLVHDFSSTNDILKVNMMGQDQKROLLEDLTRSYSGEP 174  
 Db 108 kymatsdmkdlmpgtsliv---slpvhvgepdlmwygrenefemldqlarg-grsl 163  
 Qy 175 KVIPVGMGIGKTKTAKKEYVNDSEILCRFDYAHAMATISQOHKKRELLGLHSTKMD 234  
 Db 164 evsivgmgiqgtcltakllysdpcmsrfditakavsgcyvrvnllgllstldepd 223  
 Qy 235 RVKMGAEELADMLQSLKRRRYLIVDDIWSCEVMDGVRCPTEDNKRILLTTTRND 294  
 Db 224 -----dqladrqkhkgrlylvavidltwteaawdklclfdcygn-grslllctrv 275  
 Qy 295 EVACYAGVENPCLMSFMDQESWLSFKSAFSS-ALPYEFETVGQIADDECHGLPLT 353  
 Db 276 evaaeyassgkpphmrlmndideswnllhkrifeegsyspfeanlqglalkcgsplal 335  
 Qy 354 VYVAGLL-KSKRTEDMKYAKDKSPYNDPBCSRVGLSYDHTSLDKTCLHFGI 412  
 Db 336 tvlaqlstkmgqridewqrigenvssvscapqecmrvlalsyhhlpshlkpcflfyfal 395  
 Qy 413 FPEDSDIPVKNLMRSMAEGFLKLE--NDEGEYEKCLQELVDRCLVLSKRSRDGTKIR 470  
 Db 396 ftedeqslvnelvelwpegvflneegksleevattcnelldstlfflnfgrgt-le 454  
 Qy 471 SCKVHDLIYDLCVREVORENFIINDIVLVSTPECSYLCMYKMQRPKRTGGEINYCP 530  
 Db 455 scgmhadvrelclclrear--nmhfnvyl-----yqskdq-nscq 490  
 Qy 531 GLYRALLLPVNRQLRDHNNNL-----KRTHSYF--SFHLDEPLYVYLKSEVHFKLKY 583  
 Db 491 smgrstfks--rstirlhveelawcsmseashlmjgfevcyl-----elstflvry 541  
 Qy 584 LELRHRQIDGFPRELISLIMLRYLSL-----FSYGNEDVPEICRLMNLQ 628  
 Db 542 lelglnwplfpgsvlslhlyrslfncpldqygskeavpslidlplsisslcyq 601  
 Qy 629 TFIIVQ-RFRSDI-TTFEAEIWEIMQLNHLKLPREYLPDCSSGVQGRNHDPSNLOTISV 666  
 Db 602 tfkinlfpysyflpplpsellmpqrltlcmymyyl---tshppter-vlknldp 657  
 Qy 687 LSPRCCKREYIMGIQNKKGISGNKDKYSFRDGLPNNLVYLOOLEISL----- 738  
 Db 658 lnprycgtsfrllpnllkqlvgvpedtrnsqdl---ydfrylyqleeltfrylpyaa 714



QY 739 -----ISVDYS-----LLPVIISSAKAPATLKKLTLER 767  
 Db 715 cflknapsqsgtdplrtfqtellrkeidfggtappllp-----ppdafpqsikstlrrg 770  
 QY 768 TY-LSWSYLDIYAELEPNLEVLKLMDDACCGEEMHPYMGNRKLKLLIKYSFLKWKATN 826  
 Db 771 efswakwklstlsvglpklevlllswnafigkeweeveegfphkflfidvylrwrass 830  
 QY 827 DNFPVLEMLRSCKNLKEPIEFADITHLTOLIELRECPRLGESAARIQKEDELGNRP 886  
 Db 831 dhfpylevrlrdcnrldspirdaditlaltldycqgsyvnasakqigddiqdnyss 890  
 QY 887 VDVR-----SNPLKESDSDS 902  
 Db 891 levtlrhlfpksvttvedddd 913  
 RESULT 9  
 AAU02144  
 ID AAU02144 standard; Protein: 937 AA.  
 AC AAU02144;  
 XX  
 DT 29-AUG-2001 (first entry)  
 XX  
 DE Rx 28, modified resistance protein.  
 XX  
 KW Rx: modified resistance; NBS; LRR; cell death; autoactivator;  
 KW nucleotide binding site; leucine rich repeat; pathogen resistance;  
 plant.  
 OS Solanum tuberosum.  
 OS Synthetic.  
 XX  
 PN MO200129239-A2.  
 XX  
 PD 26-APR-2001.  
 XX  
 PF 12-OCT-2000; 2000MO-GB03930.  
 XX  
 PR 15-OCT-1999; 99GB-0024483.  
 XX  
 PA (PLAN-) PLANT BIOSCIENCE LTD.  
 PI Bendahmane A, Baulcombe DC;  
 XX  
 DR WPI; 2001-290924/30.  
 XX  
 PT Modifying activation characteristics of plant resistance proteins to  
 PT produce autoactivator polypeptide capable of activation in absence of  
 PT elicitor. by introducing modifications in amino acid sequence of  
 PT protein -  
 XX  
 PS Disclosure; Page 61-65; 77pp; English.  
 XX  
 CC The sequence represents the amino acid sequence of Rx 28, a modified  
 CC resistance autoactivator. Rx encodes an NBS-LRR polypeptide having a  
 CC nucleotide binding site (NBS), leucine rich repeat (LRR), and which  
 CC mediates cellular response leading to pathogen resistance and/or cell  
 CC death or dysfunction in response to an elicitor. The Rx was modified by  
 CC introducing modification to the amino acid sequence to produce an  
 CC autoactivator polypeptide, capable of activation in absence of an  
 CC elicitor. Decoupling of resistance response from its natural elicitor is  
 CC useful for developing novel pathogen resistant plants. The modified  
 CC resistance proteins are useful for conferring resistance to non-natural  
 CC agents or stimuli and also for investigating resistance response pathways  
 CC and protein interactions e.g. with activators and repressors.  
 CC  
 XX  
 SQ Sequence 937 AA;  
 Query Match 26.0%; Score 1225.5; DB 22; Length 937;  
 Best Local Similarity 34.5%; Pred. No. 5e-98;

Matches 342; Conservative 146; Mismatches 336; Indels 167; Gaps 31;  
 QY 1 MAHASVASIMRIEISLIFNSPMQSLCDHRELCAARKVSSLEFVFNFEKN-NVREE 59  
 Db 1 mayaavtslmrtl-----hgsmeitgcd---lppfyeklsra1l---ekscimgd 47  
 QY 60 ---MTDFEVEVSAAEYRTOLRLTGVLGECNSOKKARRRRROSLOQVAEEMDHTM 116  
 Db 48 hegitlleleivevaytededmdsesrvflaqlneerstramwelfylegalcedstcv 107  
 QY 117 KESTRIODKQOVSKS- -SLVHDFSSSTNDILKVNMMVGRDOKOLLEDTFRSYGEP 174  
 Db 108 kymatsdskdlkpqtsslv---slpehdvqgenlmvgrenetemmldqarg-grel 163  
 QY 175 KVPIPIVGMGIGCTTLAKEVYNDESILCRFDVHANAYTISQNNKKEILGLHSTTKMD 234  
 Db 164 evvslvgmgigltclacklysdpcimstrfdlrakatsvqeycvnvljglstlsdcpd 223  
 QY 235 RVKMGAEALDMLQSKRRKRYLLVLDIIMSCVWDGVRGCFPRDNAGSRILTTTRMD 294  
 Db 224 -----qladrlqkhlkgrtlylvvlditweddiklcfpcyn-gsrivlttnv 275  
 QY 295 EVACYAGVENSLRMSFMDODESWSLFRSAFSS- -ALPYEFETVGOIADCHGLPLRTI 353  
 Db 276 eaeyassgkpphmrlnmfmdeswnllhkklifekegyspelenlgkqialkcgglplai 335  
 QY 354 VVVGGL- -KSKRTIEDKTVAKDVKSFTYNDPDEKSRVLSISTYHLSDLTKLHSCI 412  
 Db 336 tvlaqlskmqgrldewrigenvsvstdpcaqcmvlaslyhlpshkpcrtlylai 395  
 QY 413 FPEDSDIPIVKNLMRSMAGFELKLE- -NDLESEVKCLOELVDRLVYVSKSRGRTKR 470  
 Db 396 ftedeqisvnelvelwpegflneeegksieevatcnelldrliflfnstfgt-le 454  
 QY 471 SKVHDLIYDLCVREVOENIFIMNDIVLVSYPCCSYLCMTKMPFKRYGTDELINCPY 530  
 Db 455 scgmhdvtrrelclrear-nmmfvnvl-----rgkddq-nscag 490  
 QY 531 GLYRALILPVRKQLRDHNNMLKRTHSVFPHLEPLTYVLKSEY----- 575  
 Db 491 smgrsfks--rsrlrlh-----kvelawcrnsearslmjggfvcvle 533  
 QY 576 VHFLLKLVLELRHROIDEPREILSLIMLYSLT-----FSYGNFDPPE 620  
 Db 534 lsfklvrvldglntwptfpgsvslhlyrlslrfncplqyqgskeavpsidpils 593  
 QY 621 ICRLMNLOTFTVQ-RFNSDI-IIFAEETIWEMLQRLHLKLPRTYLPDCPSGVDKGRHLD 678  
 Db 594 lsslcylqtfklnlpfpaypffilpseallmpqrltlcmgwnyl---rsheptenr-lvl 649  
 QY 679 SNLQITISVSPRCCTKEVIMQNKIGISGNKDDYKSPFSDSGLPNNLVYLOQIEITSL 738  
 Db 650 knlqclnqlnprctgsffrlfpnlkklqvfgvpedfnsqdl---ydftrylygdeelf 706  
 QY 739 -----ISVDYS-----LLPVIISSAKAPAT 759  
 Db 707 rlypyaacflknapsqsgtdplrtfqtellrkeidfggtappllp-----ppdafpqn 762  
 QY 760 LKRLKLETTY-LSMSYLDIYAELEPNLEVLKLMDDACCGEEMHPYMGNRKLKLLIKYSF 818  
 Db 763 lksltlfigefsvawklstlsvglpklevlllswnafigkeweeveegfphkflfidvyl 822  
 QY 819 LKFKKATNDNFPVLEMLRSCKNLKEPIEFADITHLTOLIELRECPRLGESAARIQKE 878  
 Db 823 lrryrasdhfpylevrlrdcnrldspirdaditlaltldycqgsyvnasakqigdd 882  
 QY 879 QEDLGNNPVDVRI-----SNPLKESDSDS 902  
 Db 883 lqdnysseievtrhlfpksvttvedddd 913  
 RESULT 10  
 AAU02144

ID AA002146 standard; Protein: 937 AA.  
 AC AA002146;  
 DT 29-AUG-2001 (first entry)  
 DE Rx 39, modified resistance protein.  
 KW Rx; modified resistance; NBS; LRR; cell death; autoactivator;  
 KW nucleotide binding site; leucine rich repeat; pathogen resistance;  
 KW plant.  
 OS Solanum tuberosum.  
 OS Synthetic.  
 PN WO200129239-A2.  
 PD 26-APR-2001.  
 PF 12-OCT-2000; 2000WO-GB03930.  
 PR 15-OCT-1999; 99GB-0024483.  
 PA (PLAN-) PLANT BIOSCIENCE LTD.  
 PI Bendahmane A, Baulcombe DC;  
 DR WPI; 2001-290924/30.  
 DR N-PSDB; AAS03716.  
 PT Modifying activation characteristics of plant resistance proteins to  
 PT produce autoactivator polypeptide capable of activation in absence of  
 PT elicitor, by introducing modifications in amino acid sequence of  
 PT protein.  
 PS Disclosure; Page 61-65; 77pp; English.  
 XX The sequence represents the amino acid sequence of Rx 39, a modified  
 CC resistance autoactivator. Rx encodes an NBS-LRR polypeptide having a  
 CC nucleotide binding site (NBS), leucine rich repeat (LRR), and which  
 CC mediates cellular response leading to pathogen resistance and/or cell  
 CC death or dysfunction in response to an elicitor. The Rx was modified by  
 CC introducing modification to the amino acid sequence to produce an  
 CC autoactivator polypeptide, capable of activation in absence of an  
 CC elicitor. Decoupling of resistance response from its natural elicitor is  
 CC useful for developing novel pathogen resistant plants. The modified  
 CC resistance proteins are useful for conferring resistance to non-natural  
 CC agents or stimuli and also for investigating resistance response pathways  
 CC and protein interactions e.g. with activators and repressors.  
 XX  
 SQ Sequence 937 AA:

Query Match 25.9%; Score 1221.5; DB 22; Length 937;  
 Best Local Similarity 35.0%; Pred. No. 1.1e-97;  
 Matches 344; Conservative 144; Mismatches 344; Indels 151; Gaps 33;

QY 1 MAHASASIAKRTIESLTFNSPMOSCDHRELCALREKXSLPEVFKNEKN-NVNGE 59  
 DB 1 mayaaavtsimrti-----hgsmeltgcd---lqpfyeklksitrall--ekscnimgd 47  
 QY 60 ---MTDFEVEVEVSAAEYRTQLRTGLTGKNSOKKARRRROSLQOVAEDMDHIM 116  
 DB 48 hnglltleleivaytcedmwsesrnvlagnleesrismwelffylegalaisdctv 107  
 QY 117 KESTRIQDKGKOVSKR--SLVHDESSSTNDILKKNVNGRDDQKQLLEDLTRSYSGEP 174  
 DB 108 kgwmtsdsdmkdlpqtseslvr---lpehdveqpenimvqrenefemlmdqlary-grel 163  
 QY 175 KYIPVWGKIGTKTLAKRVNDESLICRPDYHAWATISOOHNNKEIILGLHSIRKMD 234  
 DB 164 evasivmgiglgkltlatklysdpcimsrfdlratavsgcyvznvllgllstlsdcp 223

QY 235 RVKMGAEELADMLQSKLRKRYLIYDDIMSCVMDVGRVCFPEEDNAGSRILLTRND 294  
 DB 224 -----dqldatrlqkhlqgrrylvividitwteawddklctfdpdy-n-gsrilllttrn 275  
 QY 295 EVACYAGVENFSLRMSFMDODESWSLFKSAAPSSP-ALPYEEYVGKQIADBCGILPTI 353  
 DB 276 evaeayassgkprhmcrlmndeswnllhkkfikegyspfeenlgkqialkcgjlpal 335  
 QY 354 VVYAGLL-KSKRTIEDMKVYAKDKSFVNNDPERCSRVLGISTYDHLTSDTLCHFGI 412  
 DB 336 tvaagllskmgqrlidewqrlgenwssvstcdpaqcmrlyalsynhlpshlpcfllyai 395  
 QY 413 FPEDSDIPYKMLRSMWMAEGFLKE--NDLEGEVEKCLQELVDRLVLVSKSRDGTIR 470  
 DB 396 ftededqsvnelvelwpvgflneegksleevattcnelldrsllfhnstfgt-le 454  
 QY 471 SCRVDHLDYLCVREVORENIFTMNDIVLDVSTPECSYLCMKRMOPFKVGTDEINCY 530  
 DB 455 scgmhvvrtrelclrear--omnfvnyl-----fgksdq-nscag 490  
 QY 531 GLYRALLTPVNRQLRDHNNNL-----KRTHSVF--SFHLEPLYVVLKSEVHFKLKV 583  
 DB 491 smgrstfs--tsrlrhkveelawcrnseahslimgfecvrl-----elsklytv 541  
 QY 584 LELRHRQIDGPREILSLIWLRYLSL-----FSYGNFVDPPEICRLMNLQ 628  
 DB 542 ldlglntwplfpgsvslshlrylsrlfpcldqygskseavpsliddplslsclyq 601  
 QY 629 TFIYVQ-RFRSDI-TIFAEEIWEIMQLRHLKLPFRFVLPDCPSGSDVKGRHLDFSNIQTSY 686  
 DB 602 tfrlnlpfpyfllpselltmpqrlrlcmgwnyl---rshpente-n-lvlnhqlcng 657  
 QY 687 LSPRCCKEYIMKIQVKKIGISGNKDDYKSPFDSGLPNMLVYLOOLETSL----- 738  
 DB 658 lnpctgtsffrlfpnlkrlqvfgvpedtrnsqdl---ydflylyqleeltrfryypaa 714  
 QY 739 -----ISDVS-----LLPVIISAKAPATLKLKLER 767  
 DB 715 cflknatpagsdqplrlfqtellhkeidfggtapclllp---ppdafpqnklstfgr 770  
 QY 768 TY-LSMSYLDIILDELPLEVYLKMDACGEEHNPVYMGFNRLKLLIKYSLFKFKAIN 826  
 DB 771 efswawkdlslygklpkllevlllswnaflygkeweeveefpnlkrlfldvlylrvass 830  
 QY 827 DNPVLELRMIRSCKNLKEPIEFADIHITQLIELRECPKLGESAAIRIQEDEDGNRP 886  
 DB 831 dhfpylevlllrcrnldspirfadlttalldidyccqsvwnsakqldqndnyss 890  
 QY 887 VDV---RISNPLK---ESDSDS 902  
 DB 891 levhttrllfpkavttvedddds 913

RESULT 11  
 AA002149  
 ID AA002149 standard; Protein: 937 AA.  
 AC AA002149;  
 DT 29-AUG-2001 (first entry)  
 DE Rx 32, modified resistance protein.  
 KW Rx; modified resistance; NBS; LRR; cell death; autoactivator;  
 KW nucleotide binding site; leucine rich repeat; pathogen resistance;  
 KW plant.  
 OS Solanum tuberosum.  
 OS Synthetic.  
 PN WO200129239-A2.  
 PD 26-APR-2001.

Query Match	25.9%	Score 1218.5	DB 22	Length 937
Best Local Similarity	35.0%	Pred.No. 2.1e-97		
Matches 344	Conservative 142	Mismatches 346	Indels 151	Gaps 32

Db 455 scgmndvtrclrclear---mmmfvrvi-----rgksdq-nscsq 496

Qy 531 GYRALLPVNRQRLDHNNNL-----KRTSVF---SFHLEPLYYLKSEVHFRLKV 588

Db 491 smgrfxfk-srrirrhkveelawcrnseashimlgfecvtl-----elsfkivr 543

Qy 584 LELRRHQIDGPPRELSTLMLRYSTL-----FSYGNPDVPEICRLNNIQ 622

Db 542 ldlglntwplfpssgvlslhlrlyslrfncplqdygskavpslidlplsslslyq 601

Qy 629 TETVVO-RRERSDI-IIFAEIEMELQRLRLKLPREFLPDPCPSGSVDKGRHLDPSNMQRTSY 686

Db 602 tfklnlpfpyyplfpseilltmpqlrtfcmgwnyl---rsheptem-lvlknlqclnq 657

Qy 687 LSPRCCTEVEVMIGIONVKKLISGKKDXYKFSRDSGLPNNLVYIQOLEILSL----- 733

Db 658 lnpfncvgsffirflpnlkklqvgfqpedefrnsqdl---ydrtrylqleelfrlyypaa 714

Qy 739 -----ISVDYS-----LPLPILISNAAFPTLKLKLER 767

Db 715 cflkntapsqtdqplrtfqtellbkeddfggtappflllp----ppdafpqnkslftfg 770

Qy 768 TY-LSWSTLIDILIAELPNLEVLKLMDDACCGEENHPIYWGFRKLLIKTSFLKFWKATN 822

Db 771 etsvawkdlslsvgklpkplevillswnatlfgkeweeveegfphklflfddvylrywtrass 830

Qy 827 DNFPLEELRLMRCKNLKEIFIEFADITHTQLIETRECPKIGESAAIRIOKEEDLGNNP 886

Db 831 dhfpylevllrdcnchdsprtdadrtllallddyqcgsvvnsakqldgdqnygss 890

Qy 887 VDVRI-----SNPLKESDSDS 902

Db 891 levhrlhflpksvltaedddd 913

RESULT 12

AAU02147

ID AAU02147 standard; Protein; 937 AA.

XX AAU02147;

XX AC

XX 29-AUG-2001 (first entry)

XX DT

XX Rx 193, modified resistance protein.

XX DE

XX Rx; modified resistance; NBS; LRR; cell death; autoactivator;

XX KW nucleotide binding site; leucine rich repeat; pathogen resistance;

XX KW plant.

XX XX

XX Solanum tuberosum.

XX OS

XX Synthetic.

XX PN

XX WO200129239-A2.

XX DD

XX 26-APR-2001.

XX XX

XX 12-OCT-2000; 2000WO-GB03930.

XX XX

XX 15-OCT-1999; 99GB-0024483.

XX XX

XX (PLAN-) PLANT BIOSCIENCE LTD.

XX PA

XX Bendahmane A, Baulcombe DC;

XX PI

XX WPI; 2001-290924/30.

XX DR

XX N-PSDB; AAS03717.

XX XX

XX Modifying activation characteristics of plant resistance proteins to

XX PT produce autoactivator polypeptide capable of activation in absence of

XX PT elicitor, by introducing modifications in amino acid sequence of

XX PT protein -

XX PS

XX Disclosure; Page 61-65; 77pp; English.

xx The sequence represents the amino acid sequence of Rx 193, a modified resistance autoactivator. Rx encodes an NBS-LRR polypeptide having a nucleotide binding site (NBS), leucine rich repeat (LRR), and which mediates cellular response leading to pathogen resistance and/or cell death or dysfunction in response to an elicitor. The Rx was modified by introducing modification to the amino acid sequence to produce an autoactivator polypeptide, capable of activation in absence of an elicitor. Decoupling of resistance response from its natural elicitor is useful for developing novel pathogen resistant plants. The modified resistance proteins are useful for conferring resistance to non-natural agents or stimuli and also for investigating resistance response pathways and protein interactions e.g. with activators and repressors.

xx Sequence 937 AA:

Query Match 25.8%; Score 1215.5; DB 22; Length 937;  
Best Local Similarity 34.9%; Pred. No. 3.8e-97;  
Matches 343; Conservative 143; Mismatches 346; Indels 151; Gaps 32;

QY 1 MAHASVASLMTIESLTFNSPMOSLSCDHREELCALREKVSLEEVYKNEKN-NVPEGE 59  
DB 1 mayasvtslmtl-----hgsmltgcd---lqpfyeklkslral--ekscnimgd 47  
QY 60 ---MTDFEVEVEVSAAEYTIQLRLTGTVLGENKSOKKARRRFRQSLQGVADMDHIW 116  
DB 48 heglilevelevaytedmdvdesrnfiaqlneesrsmwelfvlegaleclstlv 107  
QY 117 KESTIOPDKQVSK--SLVHDFSSSTNDILKKNWNGRDOROKOLEDLTFSYSGEP 174  
DB 108 kymatsmsmklkptsly---slpehdeqgeninvrgenelemmdqlarg-grel 163  
QY 175 KYIPIVGMGIGKTTTAAKEVYNDESILCRFDVHAMATISQOHKKKELLGLHSTIKMD 234  
DB 164 evasivmgigkttlaklysdpcimsrfdirakatsgcyrvnllgllstlsdepd 223  
QY 223 RKMTGEMALDMLQSLKRRKYLVLDDIWSCEWDCVRCRPFEDAGSRILLTPRND 294  
DB 224 -----qlaadrqkhlkgyrrylvlddwteadwiklcfpcyn-gsrlllttrnv 275  
QY 295 EVACYAGVENSRLRMSFMDODESWSLFRSAFSSB-ALPYEFETVKGQIADCHGLPLTI 353  
DB 276 evaeyasgskpphmrlmyfdeswnllhkkllfexgyspfenlqgalkcgqlpral 335  
QY 354 VVAVALL-KSKRTIEDMTAKDVKSEFTNDPERKSVLSDHLTSDLTCLLHRCI 412  
DB 336 tvlaqlslskmgqrldegwrlgenavsvstcpeaqcmvldlsyhlpsnlkpcfllyfat 395  
QY 413 FPEDDDIPVKNLMRSMMAEGFLKE--NDLEGEVEKCLQELVDRLVYSRKRSDGTKIR 470  
DB 396 ftededqivnelevwepglneegksleavattcnelidrsllfihfsfgt-le 454  
QY 471 SKCVHDLIYDLCREVQRBNIFFIMNDIYLVSYPCSTLCMKQKQPKRYTGDELINCPY 530  
DB 455 scgmhvvtrelclear--nmfivnl-----rgksdq-nscsq 490  
QY 531 GLYRALTPVNNRLDRDHNNNL-----KRTHSVF--SFHLEPIYVLAKSEVHPKILKY 583  
DB 491 smgrsfks--sririhveealawcrnsaahlmjgfevltl-----elstfklyrv 541  
QY 584 LELRRHQLDGPREFRILSLMLRYLSL-----FSYGNFDPVPEICRLMWLQ 628  
DB 542 ldlgintwplfsgylslhlrlsrlfnpclqgyskeavpsldipstislslylq 601  
QY 629 TFIYO-REPSDI-IIFAEIEMQLRHLKLPREYLPCCPGSGSDKGHLDPSNLQTSY 686  
DB 602 tfkllnpfsgypfllpeellmpqrltcmqwnyl---rshpeent-lvklhqlcng 657  
QY 687 LSPRCCTKIVNGIONVKKLGISGNKDKYSFRDGLNNLVLQOQLTSL-----738  
DB 658 lmpyctgsffrlfnlklqvgfyvpedfrnsqdl---ydftrylyqleellftryypaa 714

QY 739 -----ISVDYS-----LLPVIISAKAPATLKKLKER 767  
DB 715 cflknapsstqdlrrfqtellhkeidfgycapplllp-----ppdaipgnlkaltffg 770  
QY 768 TV-LSMSYLDIAELPNELEVLKMDACGCEWHPIVWGFNRKLLLYSFLKRWKATN 826  
DB 771 efavawkdslvgklpklevellismnaflgkewevveegfplkflfldgyvlyrwrss 830  
QY 827 DNPVLELRMRCKNLKPELPIEFADITHLOLIELRECPKLGESARIQKEDELDGNP 886  
DB 831 dhpyleryllrcrrldspfdadltclaldldyqgsvvnsaklqgdldnygs 890  
QY 887 VDVRI-----SNPLKESDSDS 902  
DB 891 ievthrlhfkpkvttvedddds 913

RESULT 13  
AAW48360  
ID AAW48360 standard; Protein; 1822 AA.  
XX  
AC AAW48360:  
XX  
DT 03-JUL-1998 (first entry)  
XX  
DE Tomato Prf protein.  
XX  
KW Prf; Pseudomonas syringae pv. tomato; PST; transgenic plant; fenthion;  
KW organophosphate insecticide; leucine zipper motif; immunoassay.  
XX  
Lycopodium esculentum.  
FH  
FT Key Location/Qualifiers  
FT Misc-difference 569  
FT Domain /note="Encoded by gat"  
FT Domain /label="p loop domain"  
FT Domain /label="Klnase domain 2"  
FT Domain /label="Klnase domain 3a"  
FT Domain /label="Leucine zipper"  
FT Domain /label="Leucine zipper"  
FT Region /label="Leucine-rich repeat motif"  
XX  
PN W09802545-A2.  
XX  
PD 22-JAN-1998.  
XX  
PF 10-JUL-1997; 97WO-US12022.  
XX  
PR 11-JUL-1996; 96DS-0680327.  
XX  
PA (REGC) UNIV CALIFORNIA.  
XX  
PI Oldroyd GE, Rommens C, Salmerson JM, Staskawicz BS;  
XX WPI: 1998-110592/10.  
XX DR N-PDB; AAW177777.  
XX  
DR  
XX  
PT Isolated tomato Prf nucleic acid sequences - used to produce plants  
PT which are resistant to pathogens or to confer fenthion sensitivity  
PT to plants  
XX  
PS Examples: Fig 11; 63pp; English.  
XX  
CC The present sequence is of a tomato Prf protein which contains a  
CC leucine-rich repeat, nucleotide binding and leucine zipper motifs.  
CC Prf protein has been known to be required for resistance of tomatoes  
CC against Pseudomonas syringae pv. tomato (PST). Analysis of Prf mutant  
CC alleles suggest that in addition to its role in disease resistance, the  
CC Prf protein also functions in the response of tomato to the

CC organophosphate insecticide fenithion. The invention relates to the  
 CC use of the sequence coding for Prf protein for conferring resistance in  
 CC transgenic plants to pathogens, e.g. bacteria, fungi, viruses and  
 CC nematodes. Expression of the Prf protein in cells of a fenithion  
 CC insensitive plant can be used to confer sensitivity to fenithion.  
 CC Prf polypeptides can be used to raise Prf-specific antibodies  
 CC which can be used in immunoassays for purifying Prf or for expression  
 CC cloning purposes. The invention also provides for probes and primers  
 CC based on the Prf sequence which can be used to isolate other Prf  
 CC homologs.  
 CC  
 CC  
 CC

Sequence 1822 AA;

Query Match 20.8%; Score 980; DB 19; Length 1822;  
 Best Local Similarity 30.9%; Pred. No. 4.5e-76;  
 Matches 288; Conservative 167; Mismatches 342; Indels 136; Gaps 33;

QY 26 LSCDHEELCALREKVSLEFVKNF-EKNNVFGEMDFEVEYREVASAEYTI----- 78  
 DB 970 IIdlkhdiesvkeglIclstfhdhsydehdeacqlarysvmaykxeyvIdscIay 1029  
 QY 79 -----QLRLGTVLGENKSQKKARRRFRQSLQOVAEDMDHIWKESTKI 122  
 DB 1030 shplwykvlwIsevlEnikIvkvgetce-----rnievtvhevaktttyv----- 1077  
 QY 123 QDKGKQVSKSLVHDSSSTNDILKKNMNVGDDQKQLEDLTRSYSEPR--VPIIV 180  
 DB 1078 -----apsfsayfq-----ranemegfdtdIdelkdkI---I99speldvIsIv 1119  
 QY 181 GMGIGCTTAKKENVYNDSESLCRFDYAHAMATISQOHNKKEILGLHSTKMDRVMIG 240  
 DB 1120 gmpjlgkttIakkiyndpevstfvdhagcvvqIyswreIltIIndvIepdrnk-e 1178  
 QY 241 EAELADMLQKSLRKRYLIYLDIMSCVWDGVARCPEPTEDNAGSRLLTTRNDEVACYA 300  
 DB 1179 dgeIdelIrftIktfIrlIdvtdwqkvwndIcmfsdvsnr--srIlttrIndvaeYv 1237  
 QY 301 GVNFSLRMSFMDQDESWSLFSKSAFSSSLPFEFEYVKQIDECGLPLTIYVAVGL 360  
 DB 1238 kcesdphhIrlfIddeswtIIdqevIqgescpeldevgfelskscrgIIsIvIvayvI 1297  
 QY 361 K-KRTIEDKTVAKVDKSVTNDPDERGSRVIGLSYDHLTSDIKTGLFPGFPEESDI 419  
 DB 1298 kqkktIdskvvevgsIsgfIsgIseesIs-IlgfIsYknlphYIkpIIfgfgIqgkI 1356  
 QY 420 PVKMLRSMNAEGFLKLEND--LEGEVEKCLQELVDRCLVLSKRSRDGTKRISCKVHL 477  
 DB 1357 hvskmckIwvaegfvqannekqgedagfIdIdIgrnvvmanek--rputkvtcrIhdI 1415  
 QY 478 IYDLCYREVORENIFIMNDIVLVS-----YPCSYICMTKMQPFKRVTDDELINCYGL 532  
 DB 1416 Ihkfmekakqe-----dIIdIqnsgeYfpe--rIeeyrI--fVnsydeId-----I 1460  
 QY 533 YRALPLPVNQQLDQD--DNNNLKRTHSVFSEFHELPITYLVKSEVWHKIKLVLELRHRI 591  
 DB 1461 wprsrsvrsIlnaIdpnIIdprIdsfIfe-----sfkIvkvIdlesfnI 1507  
 QY 592 DG-FPREIISLWIRYLSFSGNFDPPEICRLMNLQFPIVORFRSDIITFEIEIWEIM 650  
 DB 1508 gsfIpeIqyIlgmkYfaagtdan-sIpsIaklenIetIvrgIlgemIpc-sIikmI 1565  
 QY 651 QLEHLKLPRLYLPDCPSGSDVKGRHLDfs-----NLIQTSIYSPRCC-----TKEV 697  
 DB 1566 kIhIhiv-----ndrysIglhenmdvItgnsqIpnIetIs--trpIIfygkdaekvI 1614  
 QY 698 MGIONVKTL-----GISGNDDYKSPFSDGLPNNLVYIQQLEILISIVSYSLPVISS 752  
 DB 1615 rkmpkIrksIcIsgfIsgfYsrkIkg--rcvfrp--rIdfIshlesIkIvnsy---pakIph 1669  
 QY 753 AKAFPAFLKKLLETTYLSNSYIDIAELPNEVLKLMDDACGGEWHPIVMGFNRKLKL 812  
 DB 1670 kfnfpqIdIetIskfIrlpwtqIsIaelpnlvIkIllaIrafgdhIwevxdsefIelkYl 1729

QY 813 LIKYSFIKFWKATNDNPNVLERLMIRSCKNLKEIPFIADITHIQLIELRCPPKIGESA 872  
 DB 1730 kIdlkIkvvgwIsIdaIpIkhIvIktckIhIksIpsfIdavcIlnrvevncwvansI 1789  
 QY 873 ARIOKEQ-EDLGNPNVDRISNP--LKESDSDS 902  
 DB 1790 qdIqumqhevIandsftvItIqppdkskeqIdIs 1822

#### RESULT 14

AAW55974  
 ID AAW55974 standard; Protein; 1255 AA.

AC AAW55974;

DT 07-JUN-1999 (first entry)

XX Tomato pest resistance M1 polypeptide (copy 1).

KW Pest resistance; nematode resistance; disease resistance; M1 gene;

KW tomato; transgenic plant; crop protection; biological control.

XX Lycopersicon esculentum.

PH Key Location/Qualifiers

FT Misc-difference 178 /note="encoded by TTR"

PN MO9815171-A1.

PD 16-APR-1998.

PE 09-OCT-1997; 97WO-US18802.

PR 10-OCT-1996; 96US-0028191.

XX (REGC ) UNIV CALIFORNIA.

PA Bodeau J, Kaloshian I, Milligan S, Williamson VM;

PI Yaghoobi J;

DR WPI: 1998-240529/21.

XX N-PsDB; AAV26082.

PT Nucleic acids encoding M1 polypeptide(s) conferring nematode

PT resistance - useful to produce transgenic plants resistant to these

PT and other pests, and in marker-aided selection to assess cultivars

PT for resistance

XX Claim 12; Page 46; 55pp; English.

PS This is the amino acid sequence of a tomato M1 polypeptide that  
 CC confers resistance to nematodes such as Globodera, Heterodera and  
 CC Meloidogyne spp., and other pests such as aphids. A genetic locus,  
 CC M1, was localized by genetic analysis to a region of the tomato  
 CC genome of about 65 kb. DNA corresponding to this region was cloned  
 CC into bacterial artificial chromosome vectors. Sequence analysis of  
 CC a 52 kb BAC3 insert (see AAV26084) identified 3 open reading frames,  
 CC one of which is probably a pseudogene. By RNA blot analysis,  
 CC transcripts of approximately 4 kb corresponding to copy 1 and copy 2  
 CC were found in both resistant and susceptible tomato roots and in  
 CC leaves of resistant but not susceptible plants. cDNA sequences  
 CC corresponding to full-length transcripts of copy 1 (see AAV26082) and  
 CC copy 2 (see AAV26083) were obtained. The encoded polypeptides (see  
 CC also AAW55975) are 91% identical and contain structural features  
 CC similar to known plant resistance genes (R genes) of the nucleotide  
 CC binding site/leucine-rich repeat (NBS/LRR) family. A recombinant  
 CC expression cassette comprising an M1 polynucleotide and an operably  
 CC linked plant promoter can be used to enhance nematode resistance in  
 CC plants especially tomatoes (claimed). Antibodies raised against  
 CC M1 polypeptides can be used to screen plants for the expression of  
 CC M1 proteins.

[illegible]

Db 614 hgtlntdpldlrlrpdewellekrtftgnespdelldvgketaenckgplrvadliag 673  
QY 359 LK---KSKRTIEDWKTVAADVKSFTVNDPDERCSRVLGSLYDHLTSDKTCLHFGIPE 415  
Db 674 vlaagrektrsv-wlevgssissfllinseve-wmkvlelsydhlpkclhfaswpk 730  
QY 416 DSDIPYKNNLRSMWMAEGFLKLENDLEG--EVEKC-LOELVDRCLVLYSKRSRDGTKIRSC 472  
Db 731 dplrtlylltvygaeqfve-ktemkgyieevvxiymdliissavicfneigd--llnf 786  
QY 473 KVHDLIYDLCVREVORENIFI-----MNDIVLVDSYPE 505  
Db 787 qthdvlvhdfeclkarckenlfdtrrsapedllprqitidydeeeenhfglnfwmfdankkr 846  
QY 506 CSTLCWKYKQOPFRKRVGDEINCPYGLYRALLTPVNRQLRHDNNMLKRTSHVSFHE 565  
Db 847 hsgkhlysl---ringd-----qlddsvsd-----afhtr 873  
QY 566 PLAYVVKSEVHFKLVLELRHQY---DGPREILSLWLRYSL-----FSYGN 614  
Db 874 -----hlrlrvldlepsiwmvdsllneicmnhlrylrvtqky]pfsfn 922  
QY 615 FDVPEICRLMNQTFIVQFRSDIIFAEIWEMLQRLKLPFRYLPDCPSGSVDKGR 674  
Db 923 -----lwnleslfvsn-kgsllvllprldlvklyl-----svgacs 959  
QY 675 HLDPSNLQRTISYLSPRCCKREVIMGIQNVKLG--ISGNKDDYKSFSDSGLPNNLVYIQ 731  
Db 960 ffdmdadesllakd--tk-----lenlrllgelllsykclmnlfk--rfpn---lg 1005  
QY 732 QLEILSLISVDYS-----LLPYLISSAKA-----FPAT 759  
Db 1006 vlgfelkeswdysteqhwpfkldclelelciavgfkssnlnhcgssvatnrpwwdfhfn 1065  
QY 760 LKKIKLEERTYLSWSYLDIIAELPNLEVLKLMDDACCGEENHPYVMG---FNRLKLLIK 815  
Db 1066 lkelllydfpltsdsistiarlnlenlsydtligeevn---mgeedtfenlkflnr 1122  
QY 816 YSFLKFWKATNDNFPVLERLMIRSCNKLKEIPFADIRTLQLELRECPKLGESARI 875  
Db 1123 lltskweygeesfnpkklqcgkleeippsfgdiyslkfikivk-sqjledsalkl 1181  
QY 876 QKEQEDL-GNNPVYDV 889  
Db 1182 kkyaedmrggneiqi 1196

Search completed: September 12, 2002, 13:59:50  
Job time: 8968 sec





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 12, 2002, 11:30:22 ; Search time 27.22 Seconds  
(without alignments)  
812.093 Million cell updates/sec

Title: US-09-864-680-3

Perfect score: 4712  
1 MAHASVASIMRTIESLTFN.....PVDKRLSNPKESDSEH 905

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PCNUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4712	100.0	905	US-09-360-186-3	Sequence 3, Appli
2	980	20.8	1824	US-08-680-327-3	Sequence 3, Appli
3	980	20.8	1824	US-09-228-246-2	Sequence 2, Appli
4	852.5	18.1	1255	US-08-947-823-3	Sequence 3, Appli
5	828.5	17.6	1257	US-08-947-823-5	Sequence 5, Appli
6	667	14.2	1240	US-08-930-996A-4	Sequence 4, Appli
7	617.5	13.1	1220	US-08-930-996A-2	Sequence 2, Appli
8	565.5	12.0	429	US-09-301-085-109	Sequence 109, App
9	565.5	12.0	429	US-09-301-085-109	Sequence 109, App
10	565.5	12.0	429	PCT-US95-04589-109	Sequence 109, App
11	530	11.2	920	US-08-930-996A-8	Sequence 8, Appli
12	520	11.0	1205	US-09-330-330-1	Sequence 11, Appli
13	476	10.1	784	US-09-004-838-12	Sequence 12, Appli
14	447	9.5	1402	US-09-004-838-11	Sequence 11, Appli
15	440	9.3	885	US-08-310-912A-2	Sequence 2, Appli
16	440	9.3	885	US-08-841-089-2	Sequence 2, Appli
17	440	9.3	885	US-09-301-085-2	Sequence 2, Appli
18	440	9.3	885	PCT-US95-04589-2	Sequence 2, Appli
19	440	9.3	885	PCT-US95-04589-2	Sequence 2, Appli
20	429.5	9.1	909	US-08-310-912A-142	Sequence 142, App
21	429.5	9.1	909	US-09-301-085-142	Sequence 142, App
22	429.5	9.1	909	PCT-US95-04589-142	Sequence 142, App
23	420.5	8.9	907	US-08-930-996A-7	Sequence 7, Appli
24	382.5	8.1	416	US-09-228-246-4	Sequence 4, Appli
25	366	7.8	1074	US-09-004-838-111	Sequence 111, App
26	355	7.5	1323	US-09-004-838-90	Sequence 90, Appli
27	351	7.4	1066	US-09-004-838-24	Sequence 24, Appli

28	350	7.4	553	4	US-09-004-838-16	Sequence 16, Appli
29	336	7.1	1817	4	US-09-004-838-125	Sequence 125, App
30	330.5	7.0	1854	4	US-09-004-838-108	Sequence 108, App
31	325.5	6.9	1890	4	US-09-004-838-88	Sequence 88, Appli
32	323	6.9	1805	4	US-09-004-838-92	Sequence 92, Appli
33	321.5	6.8	1143	2	US-08-310-912A-108	Sequence 108, App
34	321.5	6.8	1143	2	US-09-301-085-108	Sequence 108, App
35	321.5	6.8	1143	5	PCT-US95-04589-108	Sequence 108, App
36	321.5	6.8	1144	1	US-08-261-663A-2	Sequence 2, Appli
37	321.5	6.8	1144	1	US-08-261-663A-4	Sequence 4, Appli
38	321.5	6.8	1144	5	PCT-US95-07754A-2	Sequence 2, Appli
39	321.5	6.8	1144	5	PCT-US95-07754A-4	Sequence 4, Appli
40	320.5	6.8	1144	3	US-08-930-996A-9	Sequence 9, Appli
41	320.5	6.8	1144	3	US-08-930-996A-10	Sequence 10, Appli
42	316.5	6.7	1366	4	US-09-004-838-92	Sequence 22, Appli
43	316	6.7	1366	4	US-09-004-838-95	Sequence 95, Appli
44	314.5	6.7	1209	5	PCT-US95-04589-107	Sequence 107, App
45	314.5	6.7	1258	2	US-08-310-912A-107	Sequence 107, App

#### ALIGNMENTS

RESULT 1  
US-09-360-186-3  
Sequence 3, Application US/09360186  
Patent No. 6262343  
GENERAL INFORMATION:  
APPLICANT: Staskawicz, et al.  
TITLE OF INVENTION: Bc2 Resistance Gene  
FILE REFERENCE: 50687  
CURRENT APPLICATION NUMBER: US/09/360,186  
CURRENT FILING DATE: 1999-07-23  
EARLIER APPLICATION NUMBER: 60/093,957  
EARLIER FILING DATE: 1998-07-23  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3  
LENGTH: 905  
TYPE: PRT  
ORGANISM: Capsicum annuum  
US-09-360-186-3

Query Match	Best Local Similarity	100.0%:	Score 4712:	DB 4:	Length 905:
Matches 905;	Conservative	0;	Mismatches	0;	Indels
0;	Gaps	0;			
QY	1 MAHASVASIMRTIESLTFNSPMOSLSCDHRELCALREKVSLEVFYKNEKNNVFGEM 60				
DB	1 MAHASVASIMRTIESLTFNSPMOSLSCDHRELCALREKVSLEVFYKNEKNNVFGEM 60				
QY	61 TDFEYEVREVASAEYTTOLRLTGTVLGSKSQKKARRRFRQSLQOVAEDMDHTKEST 120				
DB	61 TDFEYEVREVASAEYTTOLRLTGTVLGSKSQKKARRRFRQSLQOVAEDMDHTKEST 120				
QY	121 KIODGKGVSKSIVHDESSINDILKYNNVGRDOKOLLEDTFRSYSEPKYIPYV 180				
DB	121 KIODGKGVSKSIVHDESSINDILKYNNVGRDOKOLLEDTFRSYSEPKYIPYV 180				
QY	181 GNGGIGKTTIAKEVYNDESILCRFDVHAWATISQHNKKEILGLLHSTIKMDRVMKMG 240				
DB	181 GNGGIGKTTIAKEVYNDESILCRFDVHAWATISQHNKKEILGLLHSTIKMDRVMKMG 240				
QY	241 EVELADMLOKSLKRRRYLIVDDINSCFVWDVRCFPEFNAGSRILTTNDEYACYA 300				
DB	241 EVELADMLOKSLKRRRYLIVDDINSCFVWDVRCFPEFNAGSRILTTNDEYACYA 300				
QY	301 GVENSLRSPMDQESNLSKSAFSSBALYEFETVQKQIADBECHGLPLTIYVAGLL 360				
DB	301 GVENSLRSPMDQESNLSKSAFSSBALYEFETVQKQIADBECHGLPLTIYVAGLL 360				
QY	361 KSKRTIEDWKTYAKDVKSFTVNDPDRCSRVLGLSTYDHLTSLDKTCLLHFGIFPEDSDIP 420				

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Db 361 KSKRTIDMTVADVADKSYTNDPDERCSRVLGISTYDHLSDTKLHFIFEPEDSDIP 420
Qy 421 VKNLMRSMAEGFLKLNDEGEVEKLOELVDSCLVLSRSRSDGKIRSCKHDLIYD 480
Db 421 VKNLMRSMAEGFLKLNDEGEVEKLOELVDSCLVLSRSRSDGKIRSCKHDLIYD 480
Qy 481 LCAREVORENIFIMNDIVLDSYECSTYLCMKQPKRYTGDEINCPYGLYRALLTPV 540
Db 481 LCAREVORENIFIMNDIVLDSYECSTYLCMKQPKRYTGDEINCPYGLYRALLTPV 540
Qy 541 NRQLRDHNNLKRHSVSFHLERPLYVLSKSEVHFLLKYLRLHROJDFPREILS 600
Db 541 NRQLRDHNNLKRHSVSFHLERPLYVLSKSEVHFLLKYLRLHROJDFPREILS 600
Qy 601 LHMRYLSLSYGNFDPPELCRLMNTQTFIVORERSDIIFAEIWMQLRHLKLPF 660
Db 601 LHMRYLSLSYGNFDPPELCRLMNTQTFIVORERSDIIFAEIWMQLRHLKLPF 660
Qy 661 YLPDPSGSDYDKGRHLDPSNLQITISYSPRCRKEVIMGIONYKLGISGNKDDYKSPRD 720
Db 661 YLPDPSGSDYDKGRHLDPSNLQITISYSPRCRKEVIMGIONYKLGISGNKDDYKSPRD 720
Qy 721 SGLPNNLVYLQLEIISLISVDYSLLPVITISAKAPFATLKLKLERTYLSWSYLIIE 780
Db 721 SGLPNNLVYLQLEIISLISVDYSLLPVITISAKAPFATLKLKLERTYLSWSYLIIE 780
Qy 781 LPLNLEVLKMDDACCGEEMPIYMGFRKLKLLIKYSFLKFMKATNPNFYLEMLRSC 840
Db 781 LPLNLEVLKMDDACCGEEMPIYMGFRKLKLLIKYSFLKFMKATNPNFYLEMLRSC 840
Qy 841 KNLKEIPFEDADHTIQLIELRECPKLGESAAIRKOEODLGNPVDVATISNPKESDS 900
Db 841 KNLKEIPFEDADHTIQLIELRECPKLGESAAIRKOEODLGNPVDVATISNPKESDS 900
Qy 901 DSEEH 905
Db 901 DSEEH 905

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RESULT 2
US-08-680-327-3
; Sequence 3, Application US/08680327
; Patent No. 5859321
; GENERAL INFORMATION:
; APPLICANT: Staskawicz, Brian S., Oldroyd, Giles Edward,
; APPLICANT: Salmeron, John M., Rommens, Catus
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PLANT
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; ADDRESS: Winston
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/680,327
; FILING DATE: July 11, 1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/310,912
; FILING DATE: September 22, 1994
; CLASSIFICATION: 800

```

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; APPLICATION NUMBER: 08/227,360
; FILING DATE: April 13, 1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Alan. E.
; REGISTRATION NUMBER: 35,123
; REFERENCE/DOCKET NUMBER: 5151-45038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1824 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
US-08-680-327-3

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Query Match 20.8%; Score 980; DB 2; Length 1824;  
Best Local Similarity 30.9%; Pred. No. 8.7e-81;  
Matches 288; Conservative 167; Mismatches 342; Indels 136; Gaps 33;

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Qy 26 LSCDHREELCALREKVSLEFVYKNF-EKNNVGEWTFEVEYREVASAEVYT----- 78
Db 972 LIIDLKQISVYKGLCLRSFIDHFSESYDEHDEACGLARVSVMAKYAEYVIDSLAY 1031
Qy 79 -----QLRLGTVLGENKSQKKARRRFRQSLQOVAEDMDHIKKESTKI 122
Db 1032 SHPLMYKVLMISEVLENIKIVKNVGEYCE-----RRNIEVYEAHVAKTYYV----- 1079
Qy 123 QDKGQVSKESLYVDFSSSTNDILKVNKNVGRDQKOLLEDTLRSYSGEPK--VPIY 180
Db 1080 -----APESFATYQ-----RANEBMGRODTIDELDKL--LGGSPELDVIStv 1121
Qy 181 GMSGIGKTLAKEVYNDDESILCRFDYHAMATISOHNKKEILGLSLHSTIKMDRVYMG 240
Db 1122 GMPGLGKXTLAKKIYNDPEVTSRFDYHAQCVTYQVLSMRELLITLINDVLEPSDRNEK-E 1180
Qy 241 EAEIADMLQSLKRRKRLIYLDIDWISCEVNDGYARCRPTEDNAGSRLLITTRNDVACYA 300
Db 1181 DGEIADLRFRFLTKRFLIYLDVWDYKVDNLCMCFSVSNR-SRIILTRINDVAEYV 1239
Qy 301 GVENFSLRMSFMODEMSLFFKSAFSSALPYEFTVGKQIADDECHGLPLTVIVVAGL 360
Db 1240 KCESDPHHLALFRDDESWTLQKEVFGESCPRELEVDGFEISCSGLTSLSVLVAGYL 1299
Qy 361 K-SKRTEDMKTYAKDYKSVTNDPDERCSRVLGSLDYDHLTSDKTCYCLHFGIFPEDSDI 419
Db 1300 KKKKKTLDSSWKVYEOSLSORIGSLRESIS-IIGFSYKNLPHYLPCLFVYFGFLQGD 1358
Qy 420 PVKNLMRSMAEGFLKLNDE-LEGEVEKLOELVDSCLVLSRSRSDGKIRSCKHDL 477
Db 1359 HVSCKMTKLWAYEGVQANNKGGQEDTAQGLDLDIGNVMAMER-RPNKVTQCRHDL 1417
Qy 478 IYDLCAREVORENIFIMNDIVLDSY-YPCCSYLCMKQPKRYTGDEINCPYGL 532
Db 1418 LHKFCWEKAKQ-----DGLDQINSEGVPE--RLEBYRL--FVHSYDEID-----L 1462
Qy 533 YRALLPVNRQLRDH-DNNNLKRTHSVSFHLERPLYVLSKSEVHFLLKYLRLHROJ 591
Db 1463 WRPSRSNVRSLLENAPDNLMPDRDISFIE-----SFKLVKVLDESFN 1509
Qy 592 DG-FPREIISLMLRYSLSYGNFDPPELCRLMNTQTFIVORERSDIIFAEIWMQL 650
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Qy 651 QLRLKLPREFYLPDPSGSDYDKGRHLDPS-NLQITISYSPRC-----TKEVI 697
Db 1568 KLRHIV-----NDKRSGLHNMADVLTPNSQLPNETFS--TPRLFYKDKAEKYL 1616
Qy 698 MGIONVKKL-----GISGNKDDYKSPRDSGLPNNLVYLQLEIISLISVDYSLLPVITIS 752
Db 1617 RKMPLKRLKLSICPSGFGFSRKLKG-RCVRF-RLDFLSHLESLSKIVSNSY---PAKLPH 1671

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?      REGISTRATION NUMBER: 34,774
?      REFERENCE/DOCKET NUMBER: 023070-070210US
?      TELECOMMUNICATION INFORMATION:
?      TELEPHONE: (415) 576-0200
?      TELEFAX: (415) 576-0300
?      INFORMATION FOR SEQ ID NO: 3:
?      SEQUENCE CHARACTERISTICS:
?          LENGTH: 1255 amino acids
?          TYPE: amino acid
?          TOPOLOGY: linear
?      MOLECULE TYPE: protein
?      US-08-947-823-3

```

Query Match	18.1%;	Score 852.5;	DB 3;	Length 1255;
Best Local Similarity	30.1%;	Pred. No. 2.7e-69;		
Matches 274;	Conservative 156;	Mismatches 336;	Indels 145;	Gaps 34,

[illegible]

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QY      812  LLIKSYLFKFWKATNDNFVPLEETLNRSCKNLKEIPFADITHITQLELRCPKLEES  871
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1168  LNFQNGVSIKMWGESEFPNLKRLKRGCKHLEIPSPRGDIYLSKSIKYV-SQLEDS  1236
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      872  AARIQKEQEDL  882
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1227  ALKTIKEYAEDN  1237
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 5  
US-08-947-823-5

```

1 GENERAL INFORMATION:
2 APPLICANT: Williamson, Valerie M.
3 APPLICANT: Kaloshian, Isagounhi
4 APPLICANT: Yaghmoobi, Jafar
5 APPLICANT: Bodeau, John
6 APPLICANT: Milligan, Stephen
7 TITLE OF INVENTION: Procedures and Materials for Conferring
8 TITLE OF INVENTION: Pest Resistance in Plants
9 NUMBER OF SEQUENCES: 5
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: Townsend and Crew LLP
12 STREET: Two Embarcadero Center, Eighth Floor
13 CITY: San Francisco
14 STATE: California
15 COUNTRY: USA
16 ZIP: 94111-3834
17
18 COMPUTER READABLE FORM:
19 MEDIUM TYPE: Floppy disk
20 COMPUTER: IBM PC compatible
21 OPERATING SYSTEM: PC-DOS/MS-DOS
22 SOFTWARE: PatentIn Release #1.0, Version #1.30
23
24 CURRENT APPLICATION DATA:
25 APPLICATION NUMBER: US/08/947,823
26 FILING DATE: 09-OCT-1997
27
28 CLASSIFICATION: 800
29
30 PRIOR APPLICATION DATA:
31 APPLICATION NUMBER: PCT/US97/18802
32 FILING DATE: 09-OCT-1997
33
34 PRIOR APPLICATION DATA:
35 APPLICATION NUMBER: US 60/028,191
36 FILING DATE: 10-OCT-1996
37
38 ATTORNEY/AGENT INFORMATION:
39 NAME: Bastian, Kevin L.
40 REGISTRATION NUMBER: 34,774
41 REFERENCE/DOCKET NUMBER: 023070-070210US
42 TELECOMMUNICATION INFORMATION:
43 TELEPHONE: (415) 576-0200
44 TELEFAX: (415) 576-0300
45
46 INFORMATION FOR SEQ ID NO: 5:
47 SEQUENCE CHARACTERISTICS:
48 LENGTH: 1257 amino acids
49 TYPE: amino acid
50 TOPOLOGY: linear
51
52 MOLECULE TYPE: protein
53
54 US-08-947-823-5

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Query Match	17.6%	Score 828.5;	DB 3;	Length 1257;
Best Local Similarly	20.5%;	Pred. No. 4.3e-67;		
Matches 288;	Conservative 147;	Mismatches 317;		
			Indels 223;	Gaps 41;

```

07 13 ILSILFNSMOSLSODHREELICALREVSSLEFVAFNFKNVFCEMT-----DFEVE 66
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 398 LNDLBSNAISISLI---KEEL-----ELVSGELEFHSF-----FDDAEGGLYDIWAR 444
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
07 67 VREVASAEYTO--LRILTGV--LGENSKQKKARRRRQSLQVADMDHIKKE 113
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 446 VLDVAEAKQVDSILVRONGLLHLSPTTKIKLKEELISALDENIPDRGLLYVN 504
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```



```

Db      532 DGGFEKLPYLYKLEDR-----TLLETCSSVNF-----YNPLTKRVNLINILPTLSLRA 581
Qy      584 LELRHRQIDGPREI-LSLIMLRYSLSFSYGNFDVPEICRLMNLQTFIVORESDIIF 642
Db      582 LSLSHKMEELPNDLEIKLRLFRIDISRTNKRLPDSICVLYNLETLLSSCKLEELP 641
Qy      643 ABEIWMOLRHLKLPFLPDCPSGVKGRHLPDSNLQTSYLSPPRCTKEVINGION 702
Db      642 QME--KLIMLRHLDISNTWHLKMP-----LHLSRLKSLQVL---VGAKFLVGVR 686
Qy      703 VKKLGISGN-----KDYKSPRDSGLPNNLYLOLEILSLVDS----- 744
Db      687 MEDLEGNAQLYGSLSVYKLENNVDREAVKPKKREKNHVEQLSLEMSISADNSQTERD 746
Qy      745 LLEPVI-----ISSAK-----APATLKKLLEFRLYSVSY-LDIIAELPNE 785
Db      747 ILDELPRKNIQEVKIIIGRTNFPNMVADPLFLKLVKLSLNCDCYSLPALGQLPCLK 806
Qy      786 VLKL-----MODACGGEWHPIVNGFNKLKLLK 815
Db      807 FLVSGMGHGRVYVEEFYRLSSKKEPNCLEKLEFEDMTWKQWALGIG----- 856
Qy      816 YSFLKWKATNDFPYLERIMIRSCRNK-EIPIEPADITHIQLIELRCP 865
Db      857 -----EPFLLEKLSIINCPELSLEIPIQS---SLKRFVFGCP 892

```

RESULT 7  
US-08-930-996A-2  
Sequence 2, Application US/08930996A  
Patent No. 6100449

```

GENERAL INFORMATION:
APPLICANT: FIDHR, Robert
APPLICANT: ESHED, Yuval
APPLICANT: ORI, Naomi
APPLICANT: PARAN, Ilan
APPLICANT: ZAMIR, Daniel
TITLE OF INVENTION: A GENE FAMILY FROM THE 12 FUSARIUM RESISTANCE
TITLE OF INVENTION: LOCUS OF TOMATO AND USE THEREOF FOR TRANSPORTATION AND
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESS: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,996A
FILING DATE: 09-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05272
FILING DATE: 15-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 113,373
FILING DATE: 13-APR-1995
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1220 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-930-996A-2

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Query Match 13.1%; Score 617.5; DB 3; Length 1220;

```

Best Local Similarity 23.9%; Pred. No. 1,le-47;
Matches 249; Conservative 165; Mismatches 277; Indels 353; Gaps 48;
Qy      42 SLSLEFVKNFEKN---NVFGEWTEDEVEVEVAEAETIQLRLTGVLGENKSOKKA 97
Db      14 SALNVLEFRLAPAGDLLNFRKHTD-DVELEKLGILLSLQVLSD---AEKKKASNOF 69
Qy      98 RRRFROSLOQVAEDMHKE-----STKIDKGQVSKESLY--HDF-----SSST 142
Db      70 VSQWHLRLQTVADAENLEQVNYEARLRLKETSNOQVSDNLCLSDDFLNKKELEDT 129
Qy      143 NDILKKNMNVGR-----DDQ-----RKQLLEDLT--RSYSGEPK 175
Db      130 IKKLEVELEKQIGLGLKEHFISTKQETRPSPSLVDSGIFGKKNLENLVGLSLMDRK 189
Qy      176 ----VIPIVGMGIGKTTLAKEVYNDESSILCRFDVHANAATISOHNKEILGLH--- 227
Db      190 RKNLAVVPPIVGMGKTTLAKAVYNDESVOKHFGILTAMFCVSEAYDARIPKGLQETG 249
Qy      228 -STIKMD-----RVKMGAEALADK---LOSLKRRFLIYDDIWSCEV--WDGVRG 276
Db      250 STDLKADNUNLOQVRLKADNUNLOQVRLKELKRLVLDVNDVNDNYPENDLRNL 309
Qy      277 FPLEDNAGSRILLTTRNDEVACYAGVNFSLRSMFMODESNLSFR--SAFSSSEALPYE 334
Db      310 F-LQGDIGSKIIYVTRKESVALM--MDSGAIYWGILSSEDSVALFRHSLEHDKPREHE 366
Qy      335 FETVKGQIDEGCHGLPIIVVAGLLSKRTIDMKTVAKDVKSPYTNPDGCSR----- 390
Db      367 FEEVKGQIDKCKGIPRLAKALAGMLRSKSEVDENRI--LNSLETWELPS--CSNGILP 421
Qy      391 VGLSTYDHLTSDKCTCLHFGIPEPESDIPVKNLMSMAEGFLKLENDLEGEVEKLOE 450
Db      422 ALMLSTNDPLPAHLKQCLACATIPKQYQFKREYHIMLANG-----LYHGFHSGNOY 474
Qy      451 LVDRCLVIVSKNSRDGKTRSCKVHDIYDLVREYORENIFMNDIYLDVSTPECSYLC 510
Db      475 FLE-----LRSRLFEMASEPSERDVEE--FLMHLVDNLADIASNNC 516
Qy      511 MKKMQPFKRVTDGEIYWCYGLYRALLTPVNRQLRHDNNNLKR--THSVSEF---HLE 565
Db      517 I-----RLEDNKSHTLEQCRHHSYSTIGQGEFE 545
Qy      566 PLYVYLKSE-----VVA-----FKLKVLELRHRQIDGPREI- 598
Db      546 KKLSEKSEQRLRLPIDIQFHSKSLSKRVLNILPRLSLRALSLSHYQLEVLPLNDL 605
Qy      599 LSLIMLRYSLSYGNFDVPEICRLMNLQTFIVQ--RRSDIITAEIWMOL----- 652
Db      606 IKIKLRFIDLETSITKLPDSIFVLYNLETLLSCEYLEELPLQMEKILINLRHLDISN 665
Qy      653 -RHLKLP-----RF-----YLPDCPS--GS-----VDK----- 672
Db      666 TRRLKIPHLRLSLKSLQVLVGAFLVGVGRMETIAGAPMLYGSLSLELENNVDREAVK 725
Qy      673 -----GRHLDEFSNLQT---ISYLSPPRCTKEVINGIONVKKLGISGNK 712
Db      726 AKMKREKNHVEQLSLEMSISADNSQTERDILDELPH-----KNIKAVEITG-- 773
Qy      713 DDKSFRDSGLPN-----NLVYLOLEILSLISVD--YSLLEY 748
Db      774 ----YRGTFNPMVADPLFVKLVHLNLRNCKDCYSLPALGQLPEFLSIRMGHGRV 828
Qy      749 I-----ISSAKAPATLKKLLEFRLYSVSYLDIIAELPNEVLKMDACGGEWHPI 802
Db      829 TEEYGRILSSKRPF-NSLVKLRE-----DMPE-----WKQWHTL 862
Qy      803 VMGFNRLKLLIKYSPLEKFWKATNDFPYLERIMIRSCRNK-EIPIEPADIH----- 854
Db      863 GIG-----EPFLLEKLSIINCPELSLEIPIQS---SLKRLDIDC 900
Qy      855 -----TLQLELRCP 865

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Db 901 KSVTSPEFSLPTLLKRIKISGCP 924

RESULT 8  
US-08-310-912A-109

; Sequence 109, Application US/08310912A  
; Patent No. 5981730

GENERAL INFORMATION:

APPLICANT: Ausubel, Frederick M.

APPLICANT: Staskawicz, Brian J.

APPLICANT: Brent, Andrew F.

APPLICANT: Dahlbeck, Douglas

APPLICANT: Katagiri, Fumitaki

APPLICANT: Kunkel, Barbara N.

APPLICANT: Mindrinos, Michael N.

APPLICANT: Yu, Guo-Liang

TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND DETECTION

NUMBER OF SEQUENCES: 208

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2904

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30B

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/310.912A

FILING DATE: September 22, 1994

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/227,360

FILING DATE: April 13, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Leech, Karen F.

REGISTRATION NUMBER: 35,238

REFERENCE/DOCKET NUMBER: 00786/254001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 100254

INFORMATION FOR SEQ ID NO: 109:

SEQUENCE CHARACTERISTICS:

LENGTH: 429 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-310-912A-109

Query Match 12.0%; Score 565.5; DB 2; Length 429;

Best Local Similarity 32.5%; Pred. No. 1.3e-43;

Matches 143; Conservative 81; Mismatches 157; Indels 59; Gaps 12;

Db 901 KSVTSPEFSLPTLLKRIKISGCP 924

Db 157 GMPGIGTKTLAKKTYINDEVTSRFDVHAQCVVTLQYSKRELLITLINDVLEPSDRNEK-E 215

Qy 241 EAEIADMLQKSLAKRRRYLIVDDIMSCVMDGVRCEPTEEDNAGSRILLTRNDEVACYA 300

Db 216 DGEIADMLQKSLAKRRRYLIVDDIMSCVMDGVRCEPTEEDNAGSRILLTRNDEVACYA 274

Qy 301 GVENFSLRMSFMDQESNLSKSAFSEALPYEFYVGOIADBCGHLPTIYVAGL 360

Db 275 KCESDPHILRLFRDESWTLQKREVFOGESCPELEDVGFESKRSCLPLSVLVAGVL 334

Qy 361 K-SKRTIEDMKTVAKDVKSPFTNDPDERGSRVGLSTGSHLSDTKTCLHFGIPEPDSIV 419

Db 335 KKKRTTDSMKVQVQSLSSQRIQSLSEIS-IIFSPYKMLPHYLKPCFLYFGFGIQQKDI 393

Qy 420 PVKMLRSMAGFLKLEND 439

Db 394 HDSKATKILVAEEFVQANNE 413

RESULT 9

US-09-301-085-109

; Sequence 109, Application US/09301085

; Patent No. 6262248

GENERAL INFORMATION:

APPLICANT: Ausubel, Frederick M.

APPLICANT: Staskawicz, Brian J.

APPLICANT: Brent, Andrew F.

APPLICANT: Dahlbeck, Douglas

APPLICANT: Katagiri, Fumitaki

APPLICANT: Kunkel, Barbara N.

APPLICANT: Mindrinos, Michael N.

APPLICANT: Yu, Guo-Liang

TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND

TITLE OF INVENTION: DETECTION METHODS

FILE REFERENCE: 00786/254002

CURRENT APPLICATION NUMBER: US/09/301.085

CURRENT FILING DATE: 1999-04-28

EARLIER APPLICATION NUMBER: 08/310.912

EARLIER FILING DATE: 1994-09-22

EARLIER APPLICATION NUMBER: 08/227,360

EARLIER FILING DATE: 1994-04-13

NUMBER OF SEQ ID NOS: 208

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 109

LENGTH: 429

TYPE: PRT

ORGANISM: Arabidopsis thaliana

US-09-301-085-109

Query Match 12.0%; Score 565.5; DB 4; Length 429;

Best Local Similarity 32.5%; Pred. No. 1.3e-43;

Matches 143; Conservative 81; Mismatches 157; Indels 59; Gaps 12;

Db 901 KSVTSPEFSLPTLLKRIKISGCP 924







```

OY 470 RSCKVHLYLVCVREORENI-----PIMNDI-----VLVY 501
| | | | | : : : : :
DB 700 DSCQVHLMMDIAISKSTEENLVFEEGSAYIHGAIRLAISSNMKGDKSEEGIVDL 759
OY 502 SYPECYLCKYKQPKRYTGDENICPYG---LYRALLTPVNRQLRDHNNMLKRTHS 558
| | | | | : : : : :
DB 760 S--RIRLSLSE-----GDMKPFYVCKMRFIRVLDECTRGLEYHHLDDIWKINHL 808
OY 559 VFSFHLPLELYV--LKSEVYHFLKLVLELRHQRIDGEPREILSLIWLRTLSFSYGND 616
| | | | | : : : : :
DB 809 KF-LSRGCRIDLPDLGNLQOLMDIRGYVAKLPRTITKLOKLOTHAGKRTDY- 866
OY 617 VPPEICRLMNLQTFIVORESDIIFPA---EEIWMOLRLKLP-----FYLP 663
| | | | | : : : : :
DB 867 -----VWEKHSMLQRCRKVCICATCCLPLCEMYGPHKALARAOWAFACCKP 919
OY 664 DCPGSG-----SVDKG-RHL-DFSNLOITISYSPRCCKEYIMGIONAKKLGISC-NKD 713
| | | | | : : : : :
DB 920 SMTGVHEEGEAMVPGIRKLMDHLRLNINVRGNALIDIGM-LTGLHKLGVAGINKK 978
OY 714 DYKSPDSDGLPNNLVYLOOLEILSLISV-----DYSLLP-----VIISAKAP 757
| | | | | : : : : :
DB 979 NGAFKLA-----ISNKLIESLVSAGMPGLCCGLDISPPENLOSLKLYGSLKTL 1033
OY 758 ATLK-----KLEERTYLSWS--YLDIAELPNEVLKIMDACCGEEMH--PIWGFN 807
| | | | | : : : : :
DB 1034 EMIKELQHLVYKLVSTRLLEHDVAMEFLGELPKVEIIV--SPFKSEHFKRPQTGTA 1091
OY 808 RLKLLIKISFL--KFKATNDNPFVLERLMIRS-----CNKLEPIER- 850
| | | | | : : : : :
DB 1092 FVSLRYLKLAGIMGIVSEEGTMEKLELQVGRRIENIEIGFSGLEFLOININEVOLSW 1151
OY 851 -----ADHITLOLELRECPKLGESARIQKOEOLGNP 886
| | | | | : : : : :
DB 1152 FPHDHRIRAAAGADYETAMEEYQEARRKGELKKRI--REOLANP 1199

RESULT 13
US-09-004-838-12
; Sequence 12, Application US/09004838
; Patent No. 6350933
; GENERAL INFORMATION:
; APPLICANT: Michelmere, Richard W.
; APPLICANT: Shen, Kathy
; APPLICANT: Meyers, Blake
; TITLE OF INVENTION: Procedures and Materials for
; TITLE OF INVENTION: Conferring Pest Resistance in Plants
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/004,838
; FILING DATE: 09-JAN-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/781,734
; FILING DATE: 10-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Einhorn, Gregory P.
; REGISTRATION NUMBER: 38,440
; REFERENCE/DOCKET NUMBER: 023070-078810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200

```

```

; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 784 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY:
; LOCATION: 1..784
; OTHER INFORMATION: /note= "RLG1B amino acids"
; US-09-004-838-12

Query Match 10.1%; Score 476; DB 4; Length 784;
Best Local Similarity 25.3%; Pred. No. 6,1e-35;
Matches 196; Conservative 138; Mismatches 276; Indels 164; Gaps 37;

OY 19 FNSP-MOSLSCDH-REELCALREKVSLEVFVKNEFK--NNVFGEHTDFEVEYEVASAA 74
| | | | | : : : : :
DB 73 FOPIIHTYCSHRSLSXAMAEILGS-AFAVAFKELASALKRVAACVYIDKELEKN 131
OY 75 EYTIOLRLGTVLGENKSKO--KKARRPROSLQOYAEEDMIWKE-STKI-----QD 124
| | | | | : : : : :
DB 132 SSXINKK--ALLNDASQKEISKEAVKEMWLNQLHPYIDDLGLDGLATKAIHRKFSEE 187
OY 125 KGRQVSK-----ESLVHDFSSTNDILKVKNNM----- 152
| | | | | : : : : :
DB 188 YGATINKVRKLIPSCFSSSSTMRNKKIHNTSKLOELLEERNNLGLCEIGESRKLNRK 247
OY 153 -----VGRDOORKOL--EDLTRSYSGEPKVIPIYMGIGIKTTLAKEYND 197
| | | | | : : : : :
DB 248 SETSXLDPSSTVGRTRDKKELKLYEPCDRNFS--ILPIYMGIGIKTTIGRLIYDX 303
OY 198 ESTLCRFVDVAMATISQOHNKKKEILLGLHSTIKMDRYKMGIEALDM-----LQKS 251
| | | | | : : : : :
DB 304 MQVKDHFELKAWCVSDEDF--IFGISKTIFESIEG--GNQEFKDLNLQVALKEK 355
OY 252 LKKRRRLIYLDIDWISCEV--WDGVRRCFPREDNAGSRILLTTNDEYACAGYENSLSM 309
| | | | | : : : : :
DB 356 ISKRRLVYLDVWSESSTYDTEILERPF-LAGAPGSKVIITTKRLSLNQLGIDG--PYOL 413
OY 310 SFMDODEWSLFSKSAF--SSSEALPYEFETVQKQADECHGLPIYVVAAGLKSRTI 366
| | | | | : : : : :
DB 414 SDSLHNAISLSPQAHAFVANSFDSHPRI-LKPHBEGIVEKCDGLPALLIALGRLLTRKDE 472
OY 367 EDKRTYAKDVKSFTVNDPDRCSRYLGLSYDILTSDKTCLLHFGIFPEDSDIPVKLMR 426
| | | | | : : : : :
DB 473 EEWKELINS-EIWRIGKRDE-IIPXLRISYNDLSASLKFAYCSPFKDYVNRKELLI 530
OY 427 SMMABEFLKEN--DLEGEVEKLOEYDRCLVLYSKSRSDOTKIRSCKVHLLIYDLV 483
| | | | | : : : : :
DB 531 LWAABEFLNENNTKSMERLXLEYFDLLSRSEF--QHALDKSL--FVYHDLMDLMT 585
OY 484 REYORENIFIMNDIYVD--VSYPECSYLC--MYK-MQPKRYTGDENINCPGYLR 534
| | | | | : : : : :
DB 586 SYA--GDYFLRLDIEKKKALEKRYHMSFVCSBYMYKKFPEPKGAK-----KLT 634
OY 535 ALLTPYNRQLRDHNNMLKRTHSVFSFHLPELYLVKSEVYHFLKLVLELRHQRIDG 594
| | | | | : : : : :
DB 635 FLAMPV-----GMK--SWTFYLS--NKVLDLDELRLPLRLVLSYSTISKEV 679
OY 595 PREIISLWRLYLSFSYGNPFYPPICLMLNLOPI-----YQFRSDIIFAEIWE 648
| | | | | : : : : :
DB 680 PETIGMLKRLRYLNSHSTIHPENVCNLVYNQTLILGCCFTKPEPNNFL-----K 732
OY 649 LMQLRHKLPRFYLDPGSGVDKGRHLDPSNLOITISYSPRCCKEYIMGION 702
| | | | | : : : : :
DB 733 LNLRLHLD-----ISDTPOLKMKSSGIGELKNLHTLS-----KLIIIGEN 772

```

RESULT 14



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CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2904
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/310,912A
FILING DATE: September 22, 1994
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/227,360
FILING DATE: April 13, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Leach, Karen F.
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/254001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 100254
INFORMATION FOR SEQ. ID NO. 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 885 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-310-912A-2

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Query Match          9.3%; Score 440; DB 2; Length 885;
Best Local Similarity 22.6%; Pred. No. 1,5e-31;
Matches 220; Conservative 171; Mismatches 357; Indels 226; Gaps 42;

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```

QY 23 MQLSCDHEELCALREKVSLEVFVKNFEKNVFGEMTDFEVE-----VREV 70
DB 12 ISSLIYCAQVLC-----ESMMAERGHKTDLRQAITDLRIQDDGLEGRSCSNRAREW 65
QY 71 ASAEYTIQLRLTGLVGENKSSQKKARRR-----RQSLQOYAEDM 112
DB 66 LSAVQYTERKTALLVRFRRRQRTMRRRRYLSCFCADYKLOKKYSATLKSIGLERERS 125
QY 113 DHMKESTKIQDKGQVSKESLVHDFSSSTNDILKYNMVGRODKQKOLEDLTRYSIG 172
DB 126 EAIKTGGSIQVYCRREIPKS-----VGNNTTMEQVLEFL--SEEE 165
QY 173 EPRVIVPGMGIGIKTTTAKVEYNDESIL--CRFDYHAMATISOOHNKEI-----LLG 224
DB 166 ERGIIIVYGGVGKTTLMQST--NNELLITKGHOYDVLIVQMSRREGECTIOQAVGARIG 224
QY 225 LHSSTIKMDRVKMGIEAELADMLOKSLRKRRYLLVDDIWSCEVWD---GVRRCFPT 280
DB 225 L-----SMDE--KETGE--NRALKIYRALROKRFLLDDVM--EEIDLEKGTGPR--PDR 272
QY 281 DNAGSRILLTRNDDEVACAGVENFSLRMSFMDQDESMSLFKSAAFSSAL--PYEFETYG 339
DB 273 ENK--CKVMFTTRISIALCNMNGAE--YKLRYEFLEKKHAWELFCSKYWRKDLLESSSTRILA 330
QY 340 KQIADCECHGLPLTIVVAVGLLKSRTIEDMKTYAKDKSVFVNDPDER-----CSRVLGL 394
DB 331 EIVVSCGGIPLALITLIGGMAHRETEEBMIHASE-----VLTRPRAEMKGMNVVFALLKF 386
QY 395 SYDHLTSD--LKTCLLHFGLPDESDIPVKNLMRSMABEGFLKLENDLBEVEK---CLOE 450
DB 387 SYDNLESDDLRSCLFALCFPEEHSIEIQIIVEYVWGEGLTSSHG--NTIYKGYFLIGD 445
QY 451 LVDRCLVYSKRSDGTKIRSCVHDLIYDLCYREVQRENIFIMNDIYL---DVSYPECS 507
DB 446 LKAACLL-----ETGDEKTOVMKHNHVSRFALMAWSEOGTY--KELLIVPSMGHTEAP 497

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QY 508 YLCMYKMQPEKRYVNGDELINCPYGLYRALLFPVNRQLRDHNNNLKRTSHVSEFHLEPL 567
DB 498 KAENWRQALVLSLDNKRIGTLPEKLIQPKLITLMLQ-----QNSLKRITPGF----- 545
QY 568 YVVLKSEVHEKLLKYLELRHROIDGFPREILSLIMRLYSLPSYGNFDVPPETICRLMNL 627
DB 546 -----FMHMPVLRYVLDLSTSTITELPLSKIVELYELHLSMSGTKISVLPQELGNLRKL 598
QY 628 QTFIVQFRSDIILFAEIELMQLRLKLPREYLP--DCPSGSYDKGRHLDPSNLQ----- 662
DB 599 KHLIDQRTQFLQITPRDAICWLSKLEVLNLYSYAGWELQSFGEDEAEELGFADLEYLEN 658
QY 683 -----TISYLSPRCCTGEVIMGI-----QNYKKLGISG 710
DB 659 LTTGIGIVLSLETIKTLPERGALHKKHQHLEBECNELTFNLPDLTNHGRNLRSLIKS 718
QY 711 NKD-DY-----KSPRDSGLPNNLYVLOOLEILSLISVDYSLPVISSAKAFPATLKKLKL 765
DB 719 CHDELYLTPADFENDMLPS-----LEVLTLSL--HNLRCINISHC-----NKLK-- 762
QY 766 ERTYLSMSYLDITAELEPRLVLEKLMQD-----DACCGEEMHPIVWG---FNRKL----- 810
DB 763 ---NWSW-----YOKLPLEVIELEFDCREIEELISEHSESPVEDPTLFPLSKTLRTDRLP 814
QY 811 ----LLIKYSFLKFWKATNDNFPVLRMLMRSCKNLKEIPIEFADITHYQLIELRECP 866
DB 815 ELNLSILPSRFSFOK-----VETLVITNCPRYKKLP--PQERRTQMANLPYVCEE 861
QY 867 KLGESAAIRIQKEOE 880
DB 862 KMKKALEKQDPNEE 875

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Search completed: September 12, 2002, 13:57:28
Job time: 8826 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 12, 2002, 11:30:22 ; Search time 60.59 Seconds  
(without alignments)  
1435.234 Million cell updates/sec

Title: US-09-864-680-3

Perfect score: 4712

Sequence: 1 MAHASVASIMPTIESILTFN.....PVDVRIISNPKESDSEEH 905

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_71:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	980	20.8	1824	2	T07589 disease resistance
2	852.5	18.1	1255	2	T06267 nematodes resistan
3	828.5	17.6	1257	2	T06269 root-knot nematode
4	741.5	15.7	907	2	P96617 probable disease r
5	717	15.2	908	2	T48899 disease resistance
6	717	15.2	1384	2	P96573 protein F12M16.25
7	696.5	14.8	831	2	T51185 resistance protein
8	684	14.5	906	2	T48898 disease resistance
9	667	14.2	1240	2	T06404 resistance complex
10	666	14.1	899	2	H96617 probable disease r
11	653	13.9	839	2	B96538 hypothetical prote
12	652	13.8	835	2	T45590 hypothetical prote
13	651	13.8	820	2	T51186 resistance protein
14	637.5	13.5	847	2	T12977 hypothetical prote
15	636	13.5	906	2	G96621 probable disease r
16	618.5	13.1	900	2	G96617 probable disease r
17	614.5	13.0	1220	2	T06403 resistance complex
18	614	13.0	821	2	A86243 hypothetical prote
19	608.5	12.9	852	2	T08416 disease resistance
20	566	12.0	613	2	T52465 hypothetical prote
21	547.5	11.6	847	2	T12979 hypothetical prote
22	540	11.5	695	2	T52429 PRM1 homolog (limp
23	531	11.3	926	2	A57072 disease resistance
24	517.5	11.0	560	2	T52438 PRM1 homolog (limp
25	503.5	10.7	1802	2	T00020 bacterial blight-r
26	484.5	10.3	571	2	T02213 NBS-LRR type resis
27	473.5	10.0	985	2	T06049 hypothetical prote
28	458	9.7	967	2	G96637 hypothetical prote
29	457.5	9.7	919	2	T05746 hypothetical prote

30	456	9.7	889	2	C86257 resistance to Psen
31	442	9.4	889	2	F96637 hypothetical prote
32	432	9.2	921	2	D86293 F7H2.22 protein -
33	429.5	9.1	909	1	A54809 disease resistance
34	420.5	8.9	885	2	B86257 NBS/LRR disease re
35	407.5	8.6	898	2	F96659 hypothetical prote
36	407	8.6	925	2	B96638 protein T1P9.20 (i
37	406.5	8.6	941	2	H96553 hypothetical prote
38	405	8.6	389	2	T04390 NBS-LRR type resis
39	402.5	8.5	470	2	T52440 PRM1 homolog (limp
40	402.5	8.5	884	2	F96659 protein F2K11.26 (
41	392.5	8.3	483	2	T02226 NBS-LRR type resis
42	376	8.0	855	2	T05981 hypothetical prote
43	375.5	8.0	269	2	T04394 NBS-LRR type resis
44	375	8.0	892	2	T01899 disease resistance
45	374.5	7.9	313	2	T03031 NBS-LRR type resis

## ALIGNMENTS

## RESULT 1

T07589  
disease resistance protein Prf - tomato  
C/Species: Lycopersicon esculentum (tomato)  
C/Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 11-May-2000  
C/Accession: T07589  
R/Salmeron, J.M.; Oldroyd, G.E.D.; Rommens, C.M.T.; Scofield, S.R.; Kim, H.; Lavelle,  
Cell 86, 123-133, 1996  
A/Title: Tomato Prf is a member of the leucine rich repeat class of plant disease res  
A/Reference number: Z16032; M01D:96291405  
A/Accession: T07589  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 11824 <SAL>  
A/Cross-references: EMBL:065391; NID:91513143; PIDN:AAC49408.1; PID:91513144  
A/Experimental source: strain Rio Grande  
C/Genetics:  
A/Gene: Prf  
A/Map position: 5  
A/Introns: 1437/2  
C/Keywords: leucine zipper; nucleotide binding

Query Match	20.8%	Score 980;	DB 2;	Length 1824;
Best Local Similarity	30.9%	Pred. No. 2.4e-51;		
Matches 288;	Conservative 167;	Mismatches 342;	Indels 136;	Gaps 33;
QY 26	LSCDHRELCLARKVKSLEVFVKNF-EKNNVFEGMTDFEYREVAASAEYTI-----	78		
DB 972	LIIDLKQIESVKGKGLCLNSFIDHFESEYDEHDEAGGLARVASVMAKVEYIDSLAY	1031		
QY 79	-----QRLRTGYLGKNSOKKARRRFRSLOQVADMDHITKESTKI	122		
DB 1032	SHPLMYKVLMISEVLENIKIKVKNVGETCE-----RNIEVTEHVAKVTYTV-----	1079		
QY 123	ODKQKQVSKESLIVDFSSSTNDILKVKNNVGRDQKOLLEDTFRSYGEPK--VPIY	180		
DB 1080	-----APSFSAIYQ---RANEEMGFQDITIDELKDKL--LGGSPELDVI	1121		
QY 181	GMGIGKTTLAKEYYNDESILCRFDVHAMATISQHNKKETLLGLSLHTKMDRVKMG	240		
DB 1122	GMGIGKTTLAKEYYNDESILCRFDVHAMATISQHNKKETLLGLSLHTKMDRVKMG	240		
QY 241	EAEIADMLQKSLKRRRLVLDIWDIWCSEVMDGVARCPTEDMNGSRILLTRNDE	300		
DB 1181	DGEIADMLQKSLKRRRLVLDIWDIWCSEVMDGVARCPTEDMNGSRILLTRNDE	300		
QY 301	GVENFSLRMSFMDQESWLSFKSAFSEALPEFEFTVQKQIADCHGLPLTIYVAVGL	360		
DB 1240	KCESDPHHLPLFDDDESWTLQKEVFGESCPRELEVGFEISCSGGLPLSVLVAGVL	1299		
QY 361	K-SKRTIEDMKYAKDVKSFTVNDPDERCSRVLGLSYDHLTSLDKTCLLHFGIFPEDSDI	419		







QY 401 SDLTCLHFGIPEDSDIPVKNMRSMAAGFLKLENDLEGEV-----EKCLOELVDRC 455  
 Db 418 SYLHRCFLYLAHPEDHINVEKLSYCAAEIGISTADYHNGETIODVGSYLEELVRN 477  
 QY 456 LVLSKRSRDTKIRSCVHDLIYDLVREYQRENIFIMNDIVDVSYPECSYLCMTKM 515  
 Db 478 MI-IWERATASRGCTCHLHDMREVCLEFKAKEN--FLQAVASVGTSS-----526  
 QY 516 PFKRVYDGE-----INCPYGLYRALLTPVNRQLRDHNNLLKTHVSFSLHP 566  
 Db 527 -----TNSGSPCRSRLVYQCPTLH-----VERDINNKRLSLVLMHDLAVEN---572  
 QY 567 LYYVLAKSEVHFKLLKVLLELRHROIDG--FPRELSLIMLRYLSLFSGNDVPELCRL 624  
 Db 573 -WKLGTSTFRLKLLRYLDLYVDFEGMKLPFGIGNLHKLRYLSLOAKVSHLPS--L 628  
 QY 625 WNLQTFIVQFRPSDI-IIFAEIWEIM-QLRHLKLP-----REFYLP 663  
 Db 629 GNLMLLITLNDVDPEFTFVDPVFMHMLRYLKLPLMHKKTRLSLNLYKLETLVYFS 688  
 QY 664 DCPGSSVDKGRHLDPSNLQITSYLSPRCRKEV---IMGIONYKKGISGNKDYKSPR 719  
 Db 689 TWSSSKDL---CGWTRMLTALRLTRVTSLETLSASISGLRNLLEYLYVGTSH--KKMR 743  
 QY 720 DSGLPNNLVYLOQLEIILSVDSILPVIITSSAKAPATLKLKLERTYLSMYSIDIIA 779  
 Db 744 EEGI-----VDFEHLKHLLDLYMPRQOHFSPSLTFYKLESCGLEEDPMPLLE 792  
 QY 780 ELPNLEVLKMDACCCEEMHPIVWGFNRKLK-LIKYSFLFKWATNDNPFVLERMIR 838  
 Db 793 KLHLKGYILLKSGCYGRMVCSSGGFPQLKLEIVGLNKMEWLVBERGSHPLETISIL 852  
 QY 839 SCKNLKEIPIEPADIHVQLIEL 861  
 Db 853 DCEELKEIPDGLRFTYSLEVLML 875

## RESULT 5

T48899  
 disease resistance protein rp8 [similarity] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 21-Jul-2000  
 C:Accession: T48899  
 R:McDowell, J.M.; Dhandaydham, M.; Long, T.A.; Aarts, M.G.; Goff, S.; Holub, E.B.; Dangl  
 Plant Cell 10, 1861-1874, 1998  
 A>Title: Intragenic recombination and diversifying selection contribute to the evolution  
 A:Reference number: 224999; MUID:99030193  
 A:Accession: T48899  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-908 <MCD>  
 A:Cross-references: EMBL:AF089711; NID:g3901293; PIDN:AACT8631.1; PID:g3901294  
 A:Experimental source: Columbia  
 A:Gene: rp8  
 A:Introns: 293/1; 342/1  
 A:Function:  
 A:Description: susceptible allele of a gene that promotes resistance to Peronospora para

Query Match 15.2%; Score 717; DB 2; Length 908;

Best Local Similarity 26.1%; Pred. No. 9,1e-36;

Matches 252; Conservative 176; Mismatches 377; Indels 162; Gaps 32;

QY 1 MAHASVASIMRTIESLLFPNSP-MOSLSCHREELCALREYVSSLEFVKNFE-KNNVFG 58  
 Db 1 MAEAVFSGLEIKMDLRESERLOGID-----GQIDGKROLRSLOSLKADADAKKHGSD 56  
 QY 59 EMTDEVEVEREVAASAETIOLRLGTVLGENKSGCKKARR--FRGSLQVADMDHIM 116  
 Db 57 RVNRFLEVDKLDVDAEDITTESYVNLKSGKGVKKHVRRLACPLDRHRKVASDIBST 116

QY 117 KEST-----KIDCKGKOV---KESLVHDFSSSTNDILKVNKNVGRDDORKO 161  
 Db 117 KRISVEIGEMQSGIOIIGGRSLSLDERQVRQRIQRTYD--SSSEDLVGEGSVKE 174  
 QY 162 LLEDLTRSYSGEPKIPVIMGIGIKTTLAKEVYNDESILCRFDYHNAATISQHNKEI 221  
 Db 175 LVGHIVE--NDVQVYVSIAGMGIGIKTTLARQVFNHDLVRHFRDFGFAVCSQOFTQKHV 232  
 QY 222 LGLHSTIKMDRVKMGIEAEALDMLQKSLKRRKRLYLDIIMSGEVDGVRCEPRED 281  
 Db 233 WQRILOELPHDDILQMEYALQKRLQLLEAGRLVLDVWMKEDMDYKAVFPK- 291  
 QY 282 NAGSRILITFRNDEVACYAGVENFSLRMSFMDODESMLFSKSAF-----SSEALPYEE 336  
 Db 292 -RGKMKLLTSRNGCVGIHADPTCLFPRAILNPEBSMKLCERTVPRPRETEVRLDEME 350  
 QY 337 TWGQIADDECHGLPTIVVAGLLSKRTIEDKTYAKVYKSFVYN---DPDECS--R 390  
 Db 351 AMGKEWVTHCGGLPLAVKALGGLANKHVPKRVFDNIGSOIVGGSWLDNLSNSYVR 410  
 QY 391 VLGSYDHLTSDKTCQLHFGIPEDSDIPVKNMRSMAAGFLKLENDLEGEVEKLOE 450  
 Db 411 ILSLSTEDLPTHLKCFLANHPEDSEISTYSLEYMPAEGITD-GSTIEDSGEYLEE 469  
 QY 451 LVDRCLIVSKRSRDTKIRSCVHDLIYDLVREYQRENIFIMNDIVDVSYPECSYLC 510  
 Db 470 LVARNLYIADNVL-SWQSKYCCMHDMREVCLSKAKENPL---QIID--PCT-- 519  
 QY 511 MYKQPKRVYDGEINCPYGLYRALLTPVNRQLRDHNNLLKTHVSFSLH-----564  
 Db 520 -----STINQSPSRRLSI---HSGKAHHILGHKNK 549  
 QY 565 -----EPLYYVLKSEVH-EKLKYLELRHROIDG--FPRELSLIMLRYLSL 610  
 Db 550 TKYRSLIVPRFEDYWRISASVFNHTLRYLDLSWKEGCKLPSIGGLHLKRLSY 609  
 QY 611 SYGNFVPRPEICRLMNLQTFIVQFRSDI--IIFAEIWEIMQLRHLKLPFYLPDPS 667  
 Db 610 EAKVSHLP--STMRNLKLLLYLNLRVDTPEPIHVPNLKEMIQRLYSLPL-----658  
 QY 668 GSYDKGRHLDPSNLQITSY-----ISPRC---CTKRYIM 698  
 Db 659 -KMDDTKTELGLDVLNLEYLFGSTGHSSVTDLLRMTKRLRYLAVSSECKNEFTYSSIR 717  
 QY 699 GIOVKKLISGSKNDYK-SFRDGLPNNDLVYLOQLEIILSVDSYSLPVIYSSAKAP 757  
 Db 718 ELNLELNLNLEFLERYMMDYMGFEYLDHFNHKGQ---LAVRNSKLP---DQHGEP 769  
 QY 758 ATLKKLLERTYLSWSYLDIILAEPLNLEVLKMDACCCEEMHPIVWGNRLKLLI-KY 816  
 Db 770 PHLVHFLIYCGMEEDPMPLTEKLHLKSVLRKAFILSRVCSKGFQOLVIEISKE 829  
 QY 817 SPLKFWKATNDNPFVLERMIRSCNKLKEPIEFADIHVQLIEL-----RECPPL- 869  
 Db 830 SELEWIVVEEGSMPCRLTLLIDCKLKLDPGLKTLITSLKELIKGMKREKKELVPG 889  
 QY 870 ESARIQ 876  
 Db 890 EDYKVVQ 896

## RESULT 6

protein f12m16.25 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001

C:Accession: F96573

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon

Chen, C.W.; Chung, M.K.; Comai, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,

ansen, N.F.; Hughes, B.; Huitzer, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,

C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malt, R.; Marzla

```

0Y      /40 SVDLSLPLVISSAKAFPATLKRKRLKLEPTYLSNSYDIIAELPNLEVKIINDDACCEEM 799
      :  | :      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

```



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Db 98 L--KVEGQHONFSE-----TSNOQVSDPEFLINKLEDEYIEFLKDLQEOIGLIGLKE 148
QY 137 DSSSTNDILKAKNNMVGRRD--QROKLEDD-----LTSYSEEP-KVPIYMGIGTGT 188
Db 149 YFDSTKLETRPSTSLIDEPDIFGROSETEIDLRLSSGASGNLTVVPIVGMGSLGT 208
QY 189 TLAKEVYNDSEILCRPDVAMATISQOHNKEILLGLLSTTKMDRVMKAGEAELAD-- 246
Db 209 TLAKAVYNDESVMKHNHDLKAMFCVSEAYNAFRTKGLDE-----IGSIDLVYDN 258
QY 247 -----MLOSKRRKRYLLIVDDIW--SCEVWDGVRCRPTEDNAGSRILLTTRNDVAC 298
Db 259 LNOLOVYKLEKEREKEKFLIVLDVMDNNDYNEMDELNRNF--YOGDIGSKITVTRKDSVAL 317
QY 299 YAGVEFSLRMFMDDESNLSFKSAFSS-EALPY-EPEYTGKQADCHGIPLTIYV 356
Db 318 MKNGNQDIS--KGNLSTEASMSLFQRAEFENMDPMGSHLEEGROIAACCKGIPALAKTL 375
QY 357 AGLLSKRTIEDMKTVAKVYKSVFVNDPDRCSRYLGLSDHLTSDTKCLLHFGIFPED 416
Db 376 AGMLSKSFEVERKCI--LRSEIMELRNDILPALMLSTYNDLPALAKCFSCAIFPKD 432
QY 417 SDIPVKNMRSMAGFELKLENDLEGEVEKLOEVLDRCLVIVSKRSRDTKIRSCVAD 476
Db 433 YPFRKQVTHLMVANGLVVEDEI-----IOLIGNQFLELSSRS----- 472
QY 477 LIYDLCVR--EVQRENIFIMNDIVLDSYFECSTLCMTKMPKRYTGTGEINCPYGL-Y 533
Db 473 -LFEVRPNPSEGNIKELFLMHDLYNDLQALASSKLCIRLEESOGSHMLQCRHLSYSKMG 531
QY 534 RA--LLFVNR--OLRDHNNMLKRTSHVFSFHLDEPLYVYKSEVVA-----FLLLV 583
Db 532 DGFKEKTLPTLYKLEOLR-----TLPTGSSVNF-----YNPLTKVYLNILPTLSLKA 581
QY 584 LELRRHQIDGFPREI-LSLIMLRYSLSFSGNFDVPEICRYLMNLOTPIVORRSDIIF 642
Db 582 LLSHKKMEELPNDFIKLTLRFLDISRTNIKRLPDSICVLYNLFTLLSSCKLEELP 641
QY 643 ABEIMELMOLRLKLPFLPLPCPSGVKGRHLDPSNLQTSYLSPPRCTEYVINGION 702
Db 642 QME--KLIMRLHLDISNTHLMKP-----LHLSRLKSLQVL---VGAKFLVGVR 686
QY 703 VKKLISGN-----KDYKSPRDSGLPNLYLQOLETLSLSDVS----- 744
Db 687 MEDLGEAONLGSLSVYKLENNVDRREAVKPKMKREKNHVEQJSLSESEISADNSQTEPD 746
QY 745 LLPVI-----ISSAK-----AFPATLKKIKLEERTYLSWSY-LDIIAELPNLE 785
Db 747 ILDELRLPHKNIGQVAKIGRTGNFPMVADPLFLKLVKLSLNCKKCYSLPALGOLPCK 806
QY 786 VKL-----MDACCGBEHPYMGFNRLKILLIK 815
Db 807 FLTVSGMGIRVYTEEFYGRLSKRPNCLEKLEFEDEMTEKOWHMLGIG----- 856
QY 816 YSLFKFWKATNPNFVLERLIRSKCNLK-ELPIEPAHDHIOLELRSCP 865
Db 857 -----EPFLKLSIINCEPLSLPIQPS--SLKRRFVFGCP 892

```

RESULT 10  
H96617  
probable disease resistance protein PRK23.6 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001

R:Accession: H96617  
R:Theologian: A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Talion,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MID:21016719  
A:Accession: H96617  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-899 <STO>  
A:Cross-references: GB:AE005173; NID:g11034973; PIDN:AG27128.1; GSPDB:GN00141  
A:Gene: PRK23.6  
A:Map position: 1

Query Match 14.1%; Score 666; DB 2; Length 899;  
Best Local Similarity 25.5%; Pred. No. 1,1e-32;  
Matches 234; Conservative 184; Mismatches 376; Indels 124; Gaps 29;

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QY 32 EELCALREKVSLEEVKFEKNNVFGEMTDFEV-EVREVASAEYTIQLRLTGVYLG 90
Db 27 DQVTELKSNLNLKSLFKDADAKKHISEMVRHCVEELKQIVYTDIELT-----FLIK 82
QY 91 KSKK--KARRRROSL--QQAEDMDHIMKSTKIDCKOVSKESLVHDFSSTND 144
Db 83 VEMKRGIMRKIRKFASTIMDRRELASDIGISKRISKIVQDMOSFGVQOITIDGSSSH 142
QY 145 ILK-----VKNNVGRDDQKOLLEDTLSYSEPRVPIYVGMGIGTTLAK 192
Db 143 LDRORERHRTFSRDSSENFVGEAVNKKLVGLVE--KDDYVLSLTGNGGLKTTLLAR 200
QY 193 EYVNDSEILCRFVHAMATISQOHNKEILLGLHSTIKMD--DRVMKAGEAELADMLOR 250
Db 201 QVFNHNVADRFEGFAMVSQSEFTRLSVWQTLQNLTSKERDELQNMKEADLHDLFR 260
QY 251 SLKRRRYLVLDIWSCEVWDGVRCRPTEDNAGSRILLTTRNDVACVAGVENSLRMS 310
Db 261 LLESSKTLIVLDIMKEEDMDLIKPIFPK--KGMVYLLTSRSTESIAMRGDTYISFKPK 318
QY 311 FMDQDSWSLFSKAAF-----SEALPYEFYVYKQIADCHGIPLTIYVAGLAKSKRT 365
Db 319 CSTIPDSWTLFOSIAMPKRDTSFKVDEEMENKMKIKHGGSLAVKVLGGLLAKAT 378
QY 366 IEDMKTVARDVKSFV--TNDPDRCSRYLGLSDHLTSDTKCLLHFGIFPDSIDPVK 422
Db 379 LHMKRLSENIGSHYERISGNSSIDHVLVSFEELPNLTKCFILXAHFPEDHELVE 438
QY 423 NMRSMAGFELKLENDLEGEV-----EKLOELVDRCLVIVSKRSRDTKIRSCVHDL 477
Db 439 KLHYWAAEG-ISERRRYDGETIROTGDSYIELVRRNV-ISERVMTSRFEFCRLHDM 496
QY 478 IYDLCYREVQRENIFIMNDIVLDSYFECSTLCMTKMPKRYTGTGEINCPYGLR--A 535
Db 497 MREICLFKAKEENFLOIVSNHSPISMPQ-----TLGASRRV 533
QY 536 LITPVNRDLRDNHNNMLKRTSHVFSFHLDEPLYVYKSEVVAHKLKVLRLRQIDG-- 593
Db 534 LHPPTLHVRKYNKPKLSLVVYVDIGNRKMLSGSIFTRKLLRVLDVYAKKGGK 593
QY 594 PREELSLIMRLYLSFSGNFDVPEICRYLMNLOTPIVORRSDII-IFAEBIW-ELMO 651
Db 594 LPDSIDKLIHLRLYLSLKDAAKVSHPSS--LRNLVLLIYLDRTDPTDFVPMVGMRE 650
QY 652 LRHLKLPRTYLPDCPSGVKGRHLDPSNLQTSYLS--SPRCTEYVINGIONVKL-- 706
Db 651 LRLELPRP-----MHEKTLKLSNLEKLEALENFSTSSSLEDLRGMVRLFTLV 701
QY 707 -----GISG--NKDYKSFRRSGLPN-----NLVYLOLELISLISVY 743
Db 702 ILSEGISLOTLSASVGLAHLENFKIMENAGVARMGEERKAVDFTYLLKL-----TIS 757
QY 744 SLPLVIISAKAPATLKKIKLEERTYLSWSYLDIAELPNLEVYKIMLMDACCGBEHP 803
Db 758 PRLPKTI-----QHLPSHLIVLDISYCLEEDPMPILEKLELKDLSIDYLSFSGRKMVCSA 813

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QY 804 MGFRRL-KLLIKYSPFKMFKATNDNFVLERLMISCKNLKEIPFADHTLQ-LTEL 861  
 DB 814 GGFQOLKRLALDEBEMEMVVEBGSMSRLHTLSIWS-STLKEPLDGLRFTYLSKNLING 872  
 QY 862 RECPPLGESAAKIQEQ 879  
 DB 873 KSMERLSEGEFFYKVQ 890  
 RESULT 11  
 B96538  
 hypothetical protein F1413.19 [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
 C:Accession: B96538  
 R:Phenology: A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
 Chinn, C.W.; Hughes, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
 Ansen, N.F.; Hughes, B.; Hultzer, L.  
 Nature 408, 816-820, 2000  
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallon,  
 Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A:Reference number: A86141; MUID:21016719  
 A:Accession: B96538  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-839 <STO>  
 A:Cross-references: GB:AE005173; NID:95734781; PIDN:AAD50046.1; GSPDB:GN00141  
 C:Genetics:  
 A:Gene: F1413.19  
 A:Map position: 1  
 Query Match 13.9%; Score 653; DB 2; Length 839;  
 Best Local Similarity 24.9%; Pred. No. 6,4e-32;  
 Matches 234; Conservative 175; Mismatches 317; Indels 214; Gaps 34;  
 QY 1 MAHVASIMKTITSLTFNSPMQSLSCDHREICALREKSSLEVEFKNF-EKNVNGE 59  
 DB 1 MAEAVSYTVVKIQQL-LLEPFLFGIG--DQYKQLODELKRLNCFLKADDEKQHEER 57  
 QY 60 MTDEVEVEVAESAAYTIQRLTGLTVLGENKSK--KKARRF-----RSLDQVAD 111  
 DB 58 VRNNAVIGIREASVDAEDLEAF--LKAESRKQKGMKRVRLRACILNEAVSHSVGE 114  
 QY 112 MDHWTKESTKIQ---DKGQVSKESLVHDFSSSTNDLK-----VKNMVGRDQ 158  
 DB 115 IREITSRLSKTASMLDFG---IKESMGR-GLSLSDLSLRQROSPFYVVEHNLVGLSOS 170  
 QY 159 RKOLLEDFRSYSGEP-KVPIYVGSGIGTKTLAKEVYNDESILCRFVHMATISQ--- 214  
 DB 171 LEKLVDNLVS--GGEKLRVTSICMGIGLTKTLAKQIFHHKVRHFRFAMVYSQDR 228  
 QY 215 -QHNKKEILGLSLTKMDRVKMGAEALADMLQSLKRRVLYLVDDIWSCEVMDGV 273  
 DB 229 RRVHMODIFMLYSK--DENQRIILRDEQGEELHFRKRNKCLIVDDIMGKAMQCL 286  
 QY 274 RRCPTEDNAGSRILLTRNDEVACYAGVENFSLMSFMDDSEKSLKSAFSE----- 329  
 DB 287 KHPVPH--TSEIITLFRNKEVALYADPRGVLEHPOLLTCEESNELLEKISLGERNIE 344  
 QY 330 -ALYEPFETVGKQJADECHGLPLTIVVAVGLKSKRTIEDMKTYAKDVKSFTVNDPDRC 388  
 DB 345 PMLVKKMEIKQIVYRCGGPLATVIGLATKSTWNEORCENCKSTVSNCGSSNG 404  
 QY 389 SR-----VLGLSYDHLSDTKLCTLHFGIPEDSDIPVKNLMRSMWAGFL-----KL 436  
 DB 405 SKNNLVADVLTSLYEYLRPHKQCFYFAHRYEDYEYHGVGLVSCIAEGVMVPMKHEA 464  
 QY 437 ENDLGEVEKCLQELVDRCLVLSKRSRDGTRKINSCKVHDLIYDLCREVORENIFIMND 496

DB 465 GTFVEDVQDYLEELVYKSMVAVGRDITSEVMTCRHMDLAREVCLQAKOEFPVYID 524  
 QY 497 -----IVLDVSY-----PECSYLQMTOPFKRYTGDEINVCPLGRA 535  
 DB 525 SRDDEAEAFISLSTNSRRISVOLHGAEEHHTKSQEPERIDKREGTYIIYW----- 580  
 QY 536 LTFPVNRQLRDNDNNMLKRTHSVFSPFLPELYLVYKSEVHFLLKVLDELRLH-RQIDGF 594  
 DB 581 -----KLKYDYSRLVREKATVYSKILDP-----KTK-----LDLSTLRNLQQLMDF 622  
 QY 595 -----PREILSLWLYRLFSTGNEDVPPEICRLMNLQFFIYOREFSDIIFAEETWE 648  
 DB 623 PVGKNPMDLMTSLRSLSTI-----NLSS-----QNTDFVAVVSSLSKV 661  
 QY 649 LMOIRHLKLPFLYLPDCCSGSVDKGRHLD-PSNLOTISYLSPROCTKEVINGIQVKKLG 707  
 DB 662 LKRLGLTINVPCEPMLD-FVDYQVLSAFTNL-----CELEFLKLER----- 704  
 QY 708 ISGNKDYKSPRDSGLPNNLYVLOQLTSLISVDSLPIVYISSAKAPATLKLKER 767  
 DB 705 -----LPGE-----QSFSSDLGALRLMQ 722  
 QY 768 TYLSMSTYDITAEPLNLEVLKLMDA-----CGGEEMHPYMGFNRLKLLIKYSFLKF 821  
 DB 723 GGLVDDPFWLEKPLNKLQLDFESFVGSKLCSK-----NLNLEE 765  
 QY 822 WKATNDNFVLERLMISCKNLKEIPFADHTLQ-LTEL 861  
 DB 766 WTEEGAMMRLVYVLEKCNKLSVPESTRFLKNQVEI 805

## RESULT 12

T45590

hypothetical protein F12A12.50 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C&gt;Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 31-Mar-2000

C:Accession: T45590

R:Choline, N.; Robert, C.; Brothier, P.; Wincker, P.; Catolico, L.; Attiguenave, F.;

submitted to the Protein Sequence Database, December 1999

A:Reference number: 223008

A:Accession: T45590

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-835 &lt;CHO&gt;

A:Cross-references: EMBL:AL133314

A:Experimental source: cultivar Columbia; BAC clone F12A12

C:Genetics:

A:Map position: 3

A:Note: F12A12.50

C:Superfamily: disease resistance protein RPS2; leucine-rich alpha-2-glycoprotein rep

Query Match 13.8%; Score 652; DB 2; Length 835;

Best Local Similarity 25.2%; Pred. No. 7,4e-32; Indels 220; Gaps 36;

Matches 235; Conservative 164; Mismatches 314; Indels 220; Gaps 36;

QY 31 REELCALREKYSLEVEFKNEKNVFGEMT-----DEVEVEVAESAAYTIQRL 82  
 DB 28 KEDLEELTELTCIHGYLVKDYAREDEVEGSKVLVDPAVYEDVLD---TYHLK 83  
 QY 83 TGYVLGENKSKKKARRF-----RSLDQVADMDHWTKESTKIQDKGQVSKESLVHD 137  
 DB 84 -----EERSORGLRLTRNIGRMADAYSIVDDIRILKRLDITRRRETYGIGLEP 137  
 QY 138 FSSSTNDILYK-----NNMVGRDQQRQLLEDLTRSYSGEKKVPIYMGSGIG 186  
 DB 138 QGGGNTSLKRVQLRRASVDQEEVYVGLDDAKLLKLELDYDEKKNFTISIFGSGIG 197  
 QY 187 KTLTAKVEYNDESILCRPDVHAMATISQHNKKEILGLSLTKMD-----DRVAMIGA 242  
 DB 198 KTLARKIYNSRDVKEKREYRAMTYVSEQYKTGDIIMHINSIGMTSELEKIRKFADE 257









QY 592 DG--PPRELLSLIMLYLSFSGNFDVPEICRLMNLQTFIVQFRSDIIFAEIWE 648  
 DB 586 KGGKLPSSIGKLIHKLKYSLYQASTYLPSSLRNLKSL-LYNLRKINSQOLINVPNVEKE 644  
 QY 649 LMQLRHLKLPREFYLPDCPSGSVDKGRHLDFSNLOTFISYSPRCCTKEVIMGIQNVKKG- 707  
 DB 645 MLEMLYLSLP-----WERSSLTK--LELGNLKLKLETLINFSYTKDSVYDLHRMTKLRT 695  
 QY 708 ----ISGNKDDYKSPRDSGLPNNLYLLOLELSL----SVDYS----LFPYIISAKA 755  
 DB 696 LQILISG-----EGJHMETLSSALSMLGHLEDTVPSENSVOFKHPKLIYRPMLPDVQH 750  
 QY 756 PPATIKKLKLERTYLSWSYLDIIEAPNLEVLKIMDA-----CCGEWHPIVWGPNR 808  
 DB 751 FPSHLTISLYVCFLEEDMPFLKELQKLVSYWYNAYVGRMWCTGGGPPL----HR 806  
 QY 809 IKLLIKYSFLKWKATNDNPFVLERLMIRSCNKLKEPIEFADHTLOLIELR 862  
 DB 807 LEIMGCL--DALEEWIVEEGSMPLLHTLHIYDCKKLEIPDGLRIFISSIKELAIR 858

Search completed: September 12, 2002, 13:58:37  
 Job time: 8895 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 12, 2002, 13:58:42 ; Search time 31.22 Seconds  
(without alignments)  
1122.396 Million cell updates/sec

Title: US-09-864-680-3  
Perfect score: 4712  
Sequence: 1 MAHASVASIMRTESILTFN.....PYDVIRISNPLKESDSEEH 905

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues  
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	ID	Description
1	238.5	5.1	1248 1	APAF_HUMAN
2	236	5.0	1249 1	APAF_RAT
3	232.5	4.9	1249 1	APAF_MOUSE
4	186.5	4.0	1261 1	APAF_BRARE
5	152.5	3.2	1036 1	YOB6_CAEEL
6	152	3.2	1679 1	YIO9_YEAST
7	149	3.2	1692 1	CYAA_SCHPO
8	147	3.1	1928 1	CYAA_SCHPO
9	145.5	3.1	950 1	Y511_RICPR
10	143.5	3.0	3911 1	AKA9_METJA
11	139	2.9	1064 1	Y088_METJA
12	139	2.9	1828 1	CUT1_HUMAN
13	138.5	2.9	4092 1	DYHC_YEAST
14	138	2.9	2663 1	CENE_HUMAN
15	135	2.9	904 1	TLR3_HUMAN
16	134.5	2.9	1269 1	FLIH_HUMAN
17	134	2.8	2077 1	TEGU_HSV7J
18	133.5	2.8	2059 1	TEGU_HSV7J
19	133.5	2.8	2145 1	CYAA_PODAN
20	132.5	2.8	1257 1	FLIH_CAEEL
21	131.5	2.8	1427 1	REST_HUMAN
22	130.5	2.8	1428 1	YAB4_SCHPO
23	130	2.8	1046 1	SBCC_LACIA
24	130	2.8	1839 1	CYAA_SACKL
25	127.5	2.7	1256 1	FLIH_DROME
26	127	2.7	810 1	CLPC_BACSU
27	126.5	2.7	1258 1	YS00_ANASP
28	126.5	2.7	1315 1	CHAO_DROME
29	126.5	2.7	2300 1	CYAA_NEUCR
30	126	2.7	1041 1	TLR8_HUMAN
31	126	2.7	1312 1	RA50_YEAST
32	126	2.7	1727 1	ALML_SCHPO
33	125.5	2.7	2238 1	RRPL_BUNYW

34	125.5	2.7	5430 1	ACE7_HUMAN	O9upn3 homo sapien
35	125	2.7	864 1	CHEA_BORBU	O44737 borrelia bu
36	125	2.7	1169 1	SMC_METJA	O59037 methanococ
37	124.5	2.6	856 1	CLPB_HELBY	P71404 helicobacte
38	124.5	2.6	944 1	NOF1_YEAST	P32380 saccharomyc
39	124.5	2.6	959 1	IONM_HUMAN	P36776 homo sapien
40	124.5	2.6	959 1	SPCA_HUMAN	P02549 homo sapien
41	124	2.6	905 1	TR3_MOUSE	O99mb1 mus musculi
42	124	2.6	908 1	H104_YEAST	P31539 saccharomyc
43	124	2.6	2198 1	YIJ2_CAEEL	P34367 caenorhabdi
44	123.5	2.6	784 1	TLR2_MOUSE	O9gun7 mus musculi
45	123.5	2.6	1939 1	MYH6_HUMAN	P13533 homo sapien

## ALIGNMENTS

RESULT 1  
ID APAF\_HUMAN STANDARD: PRT: 1248 AA.  
AC O14727; Q9UB5; Q9UB58; Q9UB59; Q9UB61; Q9UB62; Q9UB63;  
AC Q9UB64; Q9UB65; Q9UB66; Q9UB67; Q9UB68; Q9UB69;  
AC Q9UB70; Q9UB71;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 01-MAR-2002 (Rel. 41, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Apoptotic protease activating factor 1 (Apaf-1).  
GN APAF1 OR KIA0413.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 3), AND PARTIAL SEQUENCE.  
RC TISSUE=Cervical carcinoma;  
RX MEDLINE=97410306; PubMed=9267021;  
RA Zou H., Henzel W.J., Liu X., Lutschg A., Wang X.;  
RT "Apaf-1, a human protein homologous to C. elegans CED-4, participates  
in cytochrome c-dependent activation of caspase-3.";  
RL Cell 90:405-413(1997).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 4 AND 5).  
RC TISSUE=Peripheral blood, Heart, and Cervical carcinoma;  
RX MEDLINE=99373149; PubMed=10441496;  
RA Hahn C., Hirsch B., Jahnke D., Duerkop H., Stein H.;  
RT "Three new types of Apaf-1 in mammalian cells.";  
RL Biochem. Biophys. Res. Commun. 261:746-749(1999).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RC TISSUE=T-cell;  
RX MEDLINE=99292765; PubMed=10364241;  
RA Saleh A., Striniwasula S.M., Acharya S., Fisher R., Alnemri E.S.;  
RT "Cytochrome c and dATP-mediated oligomerization of Apaf-1 is a  
prerequisite for procaspase-9 activation.";  
RL J. Biol. Chem. 274:17941-17945(1999).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Kidney;  
RX Benedict M.A., Nunez G.;  
RT submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE OF 385-1248 FROM N.A. (ISOFORM 1).  
RC TISSUE=Brain;  
RX MEDLINE=98116655; PubMed=9455477;  
RA Ishikawa K., I., Nagase T., Nakajima D., Seki N., Ohira M.,  
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;  
RT "Prediction of the coding sequences of unidentified human genes. VIII.  
78 new cDNA clones from brain which code for large proteins in  
vitro.";  
RL DNA Res. 4:307-313(1997).  
RN [6]  
RP SEQUENCE OF 810-864 AND 866-883 FROM N.A.  
RA Roberts D.L., Dalglish R., Cohen G.M., MacFarlane M.;

RT "The mammalian CED4 homologue, APAF1, exists as two distinct forms in  
 RT human cells."  
 RT Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RN [17]  
 RP SEQUENCE OF 1-138 FROM N.A. (ISOFORM 1/4/5).  
 RA Mon M., Lee J.-W., Ohn H.-H., Kim D.-U., Chung K.-S., Lee M.,  
 RA Yoo H.-S.;  
 RT "Cloning of variant Apaf1."  
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [8]  
 RP APAF-1-MEDIATED OLIGOMERIZATION.  
 RX MEDLINE-98315378; PubMed-9651578;  
 RA Srinivasula S.M., Ahmad M., Fernandes-Alnemri T., Alnemri E.S.;  
 RT "Autoactivation of procaspase-9 by Apaf-1-mediated oligomerization."  
 RT Mol. Cell 1:949-957(1998).  
 RN [9]  
 RP INDUCTION BY E2F AND P53.  
 RX MEDLINE-21283226; PubMed-11389439;  
 RA Moroni M.C., Hickman E.S., Denchi E.L., Caporaso G., Coll E.,  
 RA Cecconi F., Mueller H., Helin K.;  
 RT "Apaf-1 is a transcriptional target for E2F and p53."  
 RT Nat. Cell Biol. 3:552-558(2001).  
 RN [10]  
 RP X-RAY CRYSTALLOGRAPHY (1.3 ANGSTROMS) OF 1-97.  
 RX MEDLINE-20013059; PubMed-10543941;  
 RA Vaughn D.E., Rodriguez J., Lazebnik Y., Joshua-Tor L.;  
 RT "Crystal structure of Apaf-1 caspase recruitment domain: an alpha-  
 RT helical greek key fold for apoptotic signaling."  
 RT J. Mol. Biol. 293:439-447(1999).  
 RN [11]  
 RP STRUCTURE BY NMR OF 1-97.  
 RX MEDLINE-20047184; PubMed-10578182;  
 RA Day C.L., Dupont C., Lackmann M., Vaux D.L., Hands M.G.;  
 RT "Solution structure and mutagenesis of the caspase recruitment domain  
 (CARD) from Apaf-1."  
 RT Cell Death Differ. 6:1125-1132(1999).  
 RT -1- FUNCTION: Oligomeric Apaf-1 mediates the cytochrome c-dependent  
 RT autocatalytic activation of pro-caspase 9 (Apaf-3), leading to the  
 RT activation of caspase-3 and apoptosis. This activation requires  
 RT ATP.  
 CC -1- SUBUNIT: Monomer. Oligomerizes upon binding of cytochrome c and  
 CC dATP. Oligomeric Apaf-1 and pro-caspase-9 bind to each other via  
 CC their respective NH2-terminal CARD domains and consecutively  
 CC mature caspase-9 is released from the complex.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- ALTERNATIVE PRODUCTS: 5 isoforms; 1/Apaf-1X1 (shown here), 2/Apaf-  
 CC 1L, 3/Apaf-1S, 4/Apaf-1M and 5/Apaf-1XS; are produced by  
 CC alternative splicing.  
 CC -1- TISSUE SPECIFICITY: Ubiquitous. Highest levels of expression in  
 CC adult spleen and peripheral blood leukocytes, and in fetal brain,  
 CC kidney and lung. Isoform 1 is expressed in heart, kidney and  
 CC liver.  
 CC -1- INDUCTION: By E2F and p53 in apoptotic neurons.  
 CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 13 WD REPEATS (TRP-ASP DOMAINS).  
 CC -1- SIMILARITY: CONTAINS 1 NB-ARC DOMAIN.  
 CC -1- CAUTION: Ref.7 sequence differs from that shown due to a  
 CC frameshift in position 109.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation.  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC  
 DR EMBL; AF013263; AAC51678.1; -;  
 DR EMBL; AJ243003; CAB55579.1; -;  
 DR EMBL; AJ243004; CAB55580.1; -;  
 DR EMBL; AJ243005; CAB55581.1; -;  
 DR EMBL; AJ243006; CAB55582.1; -;  
 DR EMBL; AJ243007; CAB55583.1; -;

DR EMBL; AJ243008; CAB55584.1; -;  
 DR EMBL; AJ243009; CAB55585.1; -;  
 DR EMBL; AJ243010; CAB55586.1; -;  
 DR EMBL; AJ243011; CAB55587.1; -;  
 DR EMBL; AJ243048; CAB55588.1; -;  
 DR EMBL; AJ243107; CAB56462.1; -;  
 DR EMBL; AF134397; AAD38344.1; -;  
 DR EMBL; AF149794; AAD34016.1; -;  
 DR EMBL; AB007873; BAA24843.1; -;  
 DR EMBL; AJ133643; CAB65085.1; -;  
 DR EMBL; AJ133644; CAB65086.1; -;  
 DR EMBL; AJ133645; CAB65087.1; -;  
 DR EMBL; AF248734; AAK28401.1; ALT\_FRAME.  
 DR PDB; 1CV5; 01-DEC-99.  
 DR PDB; 1CWV; 21-JAN-00.  
 DR MTM; 602233; -;  
 DR InterPro: IPR001315; CARD.  
 DR InterPro: IPR002182; NB-ARC.  
 DR InterPro: IPR001680; WD40.  
 DR Pfam; PF00619; CARD; 1.  
 DR Pfam; PF00931; NB-ARC; 1.  
 DR Pfam; PF00400; WD40; 11.  
 DR PRINTS; PR00320; GPROTEINRPT.  
 DR SMART; SM00320; WD40; 10.  
 DR PROSITE; PS00209; CARD; 1.  
 DR PROSITE; PS00678; WD\_REPEATS\_1; 4.  
 DR PROSITE; PS00682; WD\_REPEATS\_2; 9.  
 DR PROSITE; PS00294; WD\_REPEATS\_REGION; 1.  
 DR Apoptosis; ATP-binding; Repeat; WD repeat; Alternative splicing;  
 KW 3D-structure.  
 KW DOMAIN 1  
 FT 104 415  
 FT NP\_BIND 154 161  
 FT REPEAT 613 652  
 FT REPEAT 655 694  
 FT REPEAT 697 738  
 FT REPEAT 741 780  
 FT REPEAT 796 836  
 FT REPEAT 838 877  
 FT REPEAT 880 919  
 FT REPEAT 959 998  
 FT REPEAT 1001 1040  
 FT REPEAT 1042 1080  
 FT REPEAT 1083 1122  
 FT REPEAT 1125 1164  
 FT REPEAT 1175 1212  
 FT DOMAIN 95 98  
 FT VARSPPLIC 99 109  
 FT VARSPPLIC 575 575  
 FT VARSPPLIC 824 866  
 FT VARSPPLIC 1113 1154  
 FT CONFLICT 108 108  
 FT CONFLICT 134 134  
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 FT CONFLICT 161 161  
 FT CONFLICT 370 370  
 FT CONFLICT 383 383  
 FT CONFLICT 544 544  
 FT CONFLICT 580 580  
 FT CONFLICT 608 608  
 FT CONFLICT 620 620  
 FT CONFLICT 639 639  
 FT CONFLICT 708 708  
 FT CONFLICT 742 742  
 FT CONFLICT 746 746  
 FT CONFLICT 757 757  
 FT CONFLICT 795 795  
 FT CONFLICT 798 798  
 FT CONFLICT 825 825  
 FT CONFLICT 871 871  
 FT CONFLICT 876 876  
 FT CONFLICT 949 949  
 FT CARD.  
 FT NB-ARC.  
 FT ATP (POTENTIAL).  
 FT WD 1.  
 FT WD 2.  
 FT WD 3.  
 FT WD 4.  
 FT WD 5.  
 FT WD 6.  
 FT WD 7.  
 FT WD 8.  
 FT WD 9.  
 FT WD 10.  
 FT WD 11.  
 FT WD 12.  
 FT WD 13.  
 FT POLY-SER.  
 FT MISSING (IN ISOFORM 2 AND ISOFORM 3).  
 FT E -> ETLEGESK (IN ISOFORM 5).  
 FT MISSING (IN ISOFORM 3, ISOFORM 4 AND  
 FT ISOFORM 5).  
 FT MISSING (IN ISOFORM 5).  
 FT S -> P (IN REF. 7).  
 FT N -> S (IN REF. 7).  
 FT G -> C (IN REF. 2).  
 FT S -> F (IN REF. 2; CAB55587).  
 FT Y -> T (IN REF. 2; CAB55581).  
 FT I -> R (IN REF. 2; CAB55586).  
 FT F -> L (IN REF. 2; CAB55584).  
 FT A -> T (IN REF. 2; CAB55580).  
 FT R -> C (IN REF. 2; CAB55585).  
 FT H -> R (IN REF. 2; CAB55587).  
 FT L -> F (IN REF. 2; CAB55583).  
 FT T -> A (IN REF. 2; CAB55579).  
 FT H -> R (IN REF. 2; CAB55584).  
 FT V -> A (IN REF. 2; CAB55586).  
 FT L -> P (IN REF. 2; CAB56462).  
 FT E -> G (IN REF. 2; CAB55581).  
 FT D -> A (IN REF. 2; CAB55587).  
 FT E -> G (IN REF. 2; CAB55585).  
 FT S -> T (IN REF. 2; CAB55587).  
 FT A -> L (IN REF. 2; CAB55581).  
 FT I -> V (IN REF. 2; CAB55585).

Query Match 5.1%; Score 238.5; DB 1; Length 1248;  
 Best Local Similarity 20.2%; Pred. No. 8.2e-07;  
 Matches 176; Conservative 116; Mismatches 268; Indels 313; Gaps 41;

QY 96 KARREROSLOQVAD-----MDHI-----WKESTKIQDKGKQVSK-----131  
 DB 4 KARNCLQHRALKEIKTYSIMDMHISDFLTISEEKVNEPTQOORAMLIKMLK 63  
 QY 132 -----ESTVH-----DSSSTNDILKYNMVGARD-----157  
 DB 64 DNDYSVFYNALHKGKIDLAALHDIPIVYSSSGKDSVSGITSYVTVLCGGVDPOR 123  
 QY 158 -----OROLLEDFRSTYS-----GEPKVIPIYMGIGTKTAKYENNESTIL--C-RPDVH 207  
 DB 124 VVFTRKRLVNAIQKLSKLGEGPWTITIMAGCGKSVALAEVRDHSLEGGCPGGVH 183  
 QY 208 AMATISOOHNKKEILGLHSTIMDRVKM-----IGEAELADMLQSKLRK--RYLIIV 260  
 DB 184 -WVSVGRO-DKSGILMKLQNCRLDQDESPQRLPNIIEAKRLRITIMLRKHPRLSLI 241  
 QY 261 LDIWSEVMDGVRCPPTEDNAGSRILITTRNDEVACYA-----GVE 303  
 DB 242 LDDVW--DSW--VLKAPDSQ---CQILLTRDKSVTDSVMPKRYVVPVSSLEKKEGLE 293  
 QY 304 NPSLRMSFMODESWSLFSKSAFSEALPYEFETVGKQIADCHGLPLTIYVAGLLKSK 363  
 DB 294 ILSLFVNMKRAKAD-----LPEQASHIIR---ECKSGPLVSLIGALLRD- 333  
 QY 364 RTEDMKTVAKV--KSF-----VTNDPDERCSRYLGSDYHLSJDKTCLHNGIPED 416  
 DB 334 -FPRRWETYLKQIQNKQFKIRKSSSYDYERALDEAMISIVMLMEDIKDYTTDLSTIQKD 392  
 QY 417 SDIPVKMLMSWAEGLKLENDLE-GEVEKCLQELVDRLCLVLYSKSRDGTJKRSCKVH 475  
 DB 393 VKVPTKVLCTIM-----DMETEVEDIIOEFVANKSLFC--DRNGKSPR-YLIH 438  
 QY 476 DLIYDLCVREYQRENIFIMNDIYDVSPRECSYLCMYKMQPFKRVGTGEINVCYGLYRA 535  
 DB 439 DLQVDFLETK-----NCS-----451  
 QY 536 ILTPVNRQDRDNNMLIKRTHSVSFHLEPLYVLKSEVHFILKVLRLRHQIDGFP 595  
 DB 452 -----QIQD-----LHKTIITQFYQYHOPHTLSP 475  
 QY 596 REIISLIWRLYLSFSGNEDVPEICRLMNLQTFIVQRESDIITPAEITWELMQLRHL 655  
 DB 476 DQEDCMYWNFLA-YHMASAKMHKELCALMFSLDML--KATTELVGPAHLIHEVEYKHI 532  
 QY 656 KLRFYILPDCPSGSDVGRHLDFSNLQITISLSPRCTKEVIMQIO---NYKKGISGNK 712  
 DB 533 LDEK---DCAVS-----ENQEFSLNQH-----LIGRQPPNIVQGLCE-- 570  
 QY 713 DDYKSPFSDSGLPNNLVYIQLEILSLISVDYSLPVIISAKAPATLKIKLERTYLSW 772  
 DB 571 -----PEISEVYQQAQIAQOEVOGML-----YLEW 597  
 QY 773 SYLDITIELPNEVLYKAMD---DACGGEEMHPIV-MGPNRL-----KLILITY-- 816  
 DB 598 INKNININLSLTVRPHTDVYHACFESDGRIASCGADKTLQVFAKATGKLEIKRAHE 657  
 QY 817 -SFLKEWKATNDNFPVLERLIRISCKNLKEPI 848  
 DB 658 DEVILCAFSIDDRF-----IATCSYDKKVKI 683

DE Apoptotic protease activating factor 1 (Apaf-1).  
 GN APAF1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_Taxid=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPRAIN-Sprague-Dawley;  
 RA Itoh T., Itoh A., Pleasure D.;  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP DEVELOPMENTAL REGULATION, AND INDUCTION BY BRAIN INJURY.  
 RX MEDLINE=21450943; Pubmed=11567033;  
 RA Yakovlev A.G., Ota K., Wang G., Moysesyan V., Bao W.-L., Yoshinara K.,  
 RA Faden A.I.;  
 RT "Differential expression of apoptotic protease-activating factor-1 and  
 RT caspase-3 genes and susceptibility to apoptosis during brain  
 RT development and after traumatic brain injury.";  
 RL J. Neurosci. 21:7439-7446(2001).  
 CC -1- FUNCTION: Regulates programmed cell death; necessary for normal  
 CC brain development. Participates with caspase-9 (Apaf-3) in the  
 CC cytochrome c-dependent activation of caspase-3, leading to  
 CC apoptosis. This activation requires ATP (By similarity).  
 CC -1- SUBUNIT: Monomer. Oligomerizes upon binding of cytochrome c and  
 CC dATP. Oligomeric Apaf-1 and pro-caspase-9 bind to each other via  
 CC their respective NH2-terminal CARD domains (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -1- DEVELOPMENTAL STAGE: Highly expressed in brain cortex in embryos  
 CC (E17) and new-born rats up to day 7. Very low expression  
 CC thereafter.  
 CC -1- INDUCTION: By brain injury.  
 CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 13 WD REPEATS (TRP-ASP DOMAINS).  
 CC -1- SIMILARITY: CONTAINS 1 NB-ARC DOMAIN.  
 CC -----  
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 CC -----  
 DR EMBL, AF320222; AAC35067.1; -.  
 DR InterPro: IPR001315; CARD.  
 DR InterPro: IPR002182; NB-ARC.  
 DR InterPro: IPR001680; WD40.  
 DR Pfam: PF006519; CARD. 1.  
 DR Pfam: PF009931; NB-ARC. 1.  
 DR Pfam: PF004000; WD40. 13.  
 DR PRINTS: PR00320; GPROTEINRPT.  
 DR SMART: SM00114; CARD. 1.  
 DR SMART: SM00320; WD40. 13.  
 DR PROSITE: PS50209; CARD. 1.  
 DR PROSITE: PS50294; WD\_REPEATS\_1; 4.  
 DR PROSITE: PS50082; WD\_REPEATS\_2; 9.  
 DR PROSITE: PS50294; WD\_REPEATS\_REGION; 1.  
 KW Apoptosis; ATP-binding; Repeat; WD repeat.  
 FT DOMAIN 1  
 FT 106 415 NB-ARC.  
 FT NP\_BIND 154 161 ATP (POTENTIAL).  
 FT REPEAT 613 652 WD 1.  
 FT REPEAT 655 694 WD 2.  
 FT REPEAT 697 738 WD 3.  
 FT REPEAT 741 780 WD 4.  
 FT REPEAT 796 837 WD 5.  
 FT REPEAT 838 877 WD 6.  
 FT REPEAT 880 919 WD 7.  
 FT REPEAT 959 998 WD 8.  
 FT REPEAT 1001 1040 WD 9.  
 FT REPEAT 1042 1080 WD 10.  
 FT REPEAT 1083 1122 WD 11.



DR SMART; SM00114; CARD; 1.  
 DR SMART; SM00320; WD40; 12.  
 DR PROSITE; PS50209; CARD; 1.  
 DR PROSITE; PS00678; WD\_REPEATS\_1; 4.  
 DR PROSITE; PS50082; WD\_REPEATS\_2; 9.  
 DR PROSITE; PS50294; WD\_REPEATS\_REGION; 1.  
 DR Apoptosis; ATP-binding; Repeat; WD repeat; Alternative splicing.  
 FT DOMAIN 1 90 CARD.  
 FT NP\_BIND 106 415 NB-ARC.  
 FT REPEAT 154 161 ATP (POTENTIAL).  
 FT REPEAT 613 652 WD 1.  
 FT REPEAT 655 694 WD 2.  
 FT REPEAT 697 738 WD 3.  
 FT REPEAT 741 780 WD 4.  
 FT REPEAT 796 837 WD 5.  
 FT REPEAT 838 877 WD 6.  
 FT REPEAT 880 919 WD 7.  
 FT REPEAT 959 998 WD 8.  
 FT REPEAT 1001 1040 WD 9.  
 FT REPEAT 1042 1080 WD 10.  
 FT REPEAT 1083 1122 WD 11.  
 FT REPEAT 1125 1164 WD 12.  
 FT REPEAT 1176 1213 WD 13.  
 FT VARSPLIC 99 110 GKDDGGITSEFV -> A (IN ISOFORM 2).  
 SO SEQUENCE 1249 AA; 140888 MW; 53D91539CE6025C CRC64;

Query Match 4.9%; Score 232.5; DB 1; Length 1249;  
 Best Local Similarity 24.0%; Pred. No. 1.9e-06;  
 Matches 114; Conservative 75; Mismatches 161; Indels 125; Gaps 25;

QY 96 KARRRROSLQOVAED-----MDHIMK-----ESTKIDCKGVSK----- 131  
 DB 4 KARRRROSLQOVAED-----MDHIMK-----ESTKIDCKGVSK----- 63  
 QY 132 -----ESLVR-----DFSSNDILKVNMMVGRDDQ----- 158  
 DB 64 DNCAVIFSYNNLHEGYDLAALLQSGPLVSSSGKDTGIGTSFVTVLCGGVQRP 123  
 QY 159 -----KROLEDLTR-----SYSGEKVPIYVGMGIGTKTTAKVEYNDSIL--CFEDVHA 208  
 DB 124 VIEFTRKLVHAIOOKLMKLMKGEPGWVYIYMACGKSVLAEEVVRHSLLEGCGSGGVH 183  
 QY 209 WATISQOHKKKEILLGLSTIKMDRVKM-----IGEAELADMLQSLKKR--RYLIVL 261  
 DB 184 WVSIGKQ-DKSGGLMKLQNLCKRIDDDESFQRLPINEEKKRLRYLMLKRRSLIL 242  
 QY 262 DDIVSCVWDGVRRCFPTEDNAGSRILLTTRNDEVA--CYAGVENFSLMSFMDQ--ES 317  
 DB 243 DDVW--DPM--VLKAF--DNO--COILLTRDKSVTDSVMGPKHVPEVSGIGREKLEI 294  
 QY 318 WSLFSAFSEALPYEFETGKQIADDECHGLPLTIYVALLLS-----KTIID- 368  
 DB 295 LSLFVN--MKEDLPAAEHSTIK--ECKGSPVLSLIGALLDFPRMAVYLRQOLNK 348  
 QY 369 -WKTAVDVKSFVNDPDERCSRVLGSLYDHLTSDKTLHFGIFPDSIDIPVKNLRS 427  
 DB 349 QFKRIRK-----SSYDEALDEAMSTISYEMLRDINDYITDLQKDVAPTKVLCYL 403  
 QY 428 WMAEGFLKLENDL-GEVEKCLQELVDRCLVLSKRSRDKGKIRSC-KVHDLIYD 480  
 DB 404 W-----DLTEVEEDILQEFVNSKSLFCNRNGK-----FCYLLHDLQVD 443

RESULT 4  
 APAF\_BRARE STANDARD; PRT; 1261 AA.  
 ID APAF\_BRARE  
 AC Q919H8;  
 DT 01-MAR-2002 (Rel. 41, Created)  
 DT 01-MAR-2002 (Rel. 41, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 GN Apoptotic protease activating factor 1 (Apaf-1).  
 DN APAF1.

OS Brachydanio rerio (zebrafish) (zebra danio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
 OC Cypriniformes; Cyprinidae; Rasbora; Danio.  
 RN NCBI\_TaxID=7955;  
 RP [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20373792; PubMed=10917738;  
 RA Inohara N., Nunez G.;  
 RT "Genes with homology to mammalian apoptosis regulators identified in  
 RT zebrafish."  
 RL Cell Death Differ. 7:509-510(2000).  
 CC -! FUNCTION: Oligomeric Apaf-1 mediates the cytochrome c-dependent  
 CC autocatalytic activation of pro-caspase 9 (Apaf-3), leading to the  
 CC activation of caspase-3 and apoptosis. This activation requires  
 CC ATP (By similarity).  
 CC -! SUBUNIT: Monomer. Oligomerizes upon binding of cytochrome c and  
 CC dATP (By similarity).  
 CC -! SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -! SIMILARITY: CONTAINS 1 CARD DOMAIN.  
 CC -! SIMILARITY: CONTAINS 13 WD\_REPEATS (TRP-ASP DOMAINS).  
 CC -! SIMILARITY: CONTAINS 1 NB-ARC DOMAIN.  
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 CC -----  
 CC EMBL: AF251502; AAF67189.1; -;  
 CC ZFIN; ZDB-GENE-000616-4; apaf1.  
 CC InterPro; IPR001315; CARD.  
 CC InterPro; IPR002182; NB-ARC.  
 CC InterPro; IPR001680; WD40.  
 CC Pfam; PF00619; CARD; 1.  
 CC Pfam; PF00931; NB-ARC; 1.  
 CC Pfam; PF00400; WD40; 12.  
 CC PRINTS; PR00320; GPROTEINRPT.  
 CC SMART; SM00114; CARD; 1.  
 CC SMART; SM00320; WD40; 11.  
 CC PROSITE; PS50209; CARD; 1.  
 CC PROSITE; PS00678; WD\_REPEATS\_1; 2.  
 CC PROSITE; PS50082; WD\_REPEATS\_2; 7.  
 CC PROSITE; PS50294; WD\_REPEATS\_REGION; 1.  
 CC Apoptosis; ATP-binding; Repeat; WD repeat.  
 KW DOMAIN 1 90 CARD.  
 FT NP\_BIND 106 417 NB-ARC.  
 FT REPEAT 154 161 ATP (POTENTIAL).  
 FT REPEAT 615 654 WD 1.  
 FT REPEAT 657 696 WD 2.  
 FT REPEAT 700 743 WD 3.  
 FT REPEAT 746 785 WD 4.  
 FT REPEAT 798 836 WD 5.  
 FT REPEAT 840 879 WD 6.  
 FT REPEAT 882 921 WD 7.  
 FT REPEAT 964 1003 WD 8.  
 FT REPEAT 1006 1045 WD 9.  
 FT REPEAT 1047 1088 WD 10.  
 FT REPEAT 1091 1130 WD 11.  
 FT REPEAT 1133 1172 WD 12.  
 FT REPEAT 1184 1223 WD 13.  
 SO SEQUENCE 1261 AA; 142933 MW; F80CC9CB41764F1C CRC64;

Query Match 4.0%; Score 186.5; DB 1; Length 1261;  
 Best Local Similarity 20.7%; Pred. No. 0.0011;  
 Matches 116; Conservative 80; Mismatches 187; Indels 177; Gaps 27;

QY 94 KKKARRRROSLQOVAED-----MDHIMKESKTKQDK-----GQVSKK----- 132  
 DB 2 EERRARRRRLRSKATLEQDIKASVLDHMTISDGLVLTNDEARVLSKATRKQDAVALLETLL 61

QY 133 -----SLVHD-----FSSSTNDILKYNMV 153  
 DB 62 KRDNRAYISFYNNALLRESYGLDASLHSDLPILSPBEGKSPADGVSFVQALIS-----V 116  
 QY 154 GRDDQR-----QLEDLTRSYSGEPYVIPVGMGIGKTTLAKEYNDESIL- 201  
 DB 117 GVPQRPVFEVSRPPLNLRIRRELYQRLDPTGCVTVFGMAGSGKSVMAAEVVRDRLIKE 176  
 QY 202 CRDVNAAATISQHNKKRILLGLHSTFKMDRVMKIGALADMLQK----- 250  
 DB 177 CEPDGVHMLSVG-QCERADL-----VRMOSLCFRLEQCCSDPTSQRPSTVEAKER 228  
 QY 251 -----SLKR-KRYLIVDDIMSCVMDVGRCPPTEDNAGSRILTTNRN-----DEYACYAG 301  
 DB 229 LRFLMRRPRRSLILDDVMD-----SSLSRSPDIQ-----CRVLLTTRNALDVSF-----SG 277  
 QY 302 VENESLRMSFMDQESWLSFKSAFSSSEALPYEFETVGKQIADCHGLPLTIVVAGLKL 361  
 DB 278 VREYEVENGDLDEKALEIL-----ALYVNGMKMKLPEQARSIVSECKSPFLVVSILGALLR 334  
 QY 362 S-----KRTIEDMKTVAKDVKSFTYNDPERCS-----RVLGISYDHLTSDLKTCL 408  
 DB 335 EEPDRMSYLRLOQOKFRIRKS-SSYDYEALDQAMDASLQVLEAEHOELTRDL----- 388  
 QY 409 HEGIFPEDSDIPYKNLMRSMMAEGFLKLENDLEGEYEKCLQELVDRCLVLSKRSRDGK 468  
 DB 389 --SVMKDKIKVPAKVLSTVM-----GLELE-----EVEDVLOEFVAKSL- 426  
 QY 469 INSCK-----VHDLIYLCVREVORENIFIMNDIVLVSYPECSYLCMYMPKRYT 521  
 DB 427 FRDCNORPRYRYLHDLQDF-LAEONRDOIAELHKMVR-----QYGRFYSKRPPDSAD 479  
 QY 522 GDEI-----NYCPGYLRAILF 538  
 DB 480 KSLIYVYQFPIYMAKAGLS 499  
 RESULT 5  
 YOB6 CAEEL STANDARD: PRT: 1036 AA.  
 AC 009259;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Hypothetical 118.2 kDa protein C30G12.6 in chromosome II.  
 GN C30G12.6.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 NC NCB1\_Taxid=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA Latreille P.;  
 RL Submitted (Jul-1995) to the EMBL/GenBank/DBJ databases.  
 RL  
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 CC  
 DR EMBL: U21319; AAC46675.1; -  
 DR Wormpep: C30G12.6; CE01837.  
 KW Hypothetical protein.  
 SQ SEQUENCE 1036 AA; 118234 MW; FE5A40D301780B82 CRC64;

Query Match 3.2%; Score 152.5; DB 1; Length 1036;  
 Best Local Similarity 18.9%; Pred. No. 0.099;

Matches 177; Conservative 137; Mismatches 277; Indels 347; Gaps 46;  
 QY 118 ESTYIQQKGVKSVKESLVHDFSSSTNDILKYNMVRGRD-----QRKL----- 162  
 DB 37 DSQFASSKANEPQNDSDPERQSS-----VSKQSDANDEDEINEVIOEOKELDNEEDFN 93  
 QY 163 -----LEDLTR-----SYGEPYVIPVGMGIGKTTLAKEYNDESILCRD 205  
 DB 94 LRTIEEVLVDVLFARIRRVFEVYRAEPALALFDVA-----HKIRKSTMLCKRN 146  
 QY 206 VHAATISQHNKKRILLGLHSTFKMDR-----VKNIGAEALADMLQSLKR 254  
 DB 147 -----TVID-----SILEGL--SIVDERRQDGAEEAHLVITAKLA-TKNSMKC 193  
 QY 255 K-----RYLIVDDIMSCVMDVGRCPPTEDNAGSRILTTNRNDEVACYAGVENSILR 308  
 DB 194 SDLYKLLILVDRILYLA--DSFYRC-----RIVRLIACMEANRYAYV----- 236  
 QY 309 MSFMDQESWLSFKSAFSSSEALPYEFETVGKQIADCHGLPLTIVVAGLKSRTIED 368  
 DB 237 MREHGD-----AFLSDEDPTESE-----VMIPSGVNR----- 265  
 QY 369 MKTVAKDVKSFTYNDPERCSRVLGLS-YDHLTSDLKT-----LHFGIFPEDSDI 419  
 DB 266 W--MGLAKSLDDKSPEYRCACAVATALSMDHDIJCKTTCODEVTYNDLKLKSVHVDSEY 323  
 QY 420 PVKNLMRSMMAEGFLKLENDLEGEYEKCLQELVDRCLVLSKRSRDGKIRSCVHDLIY 479  
 DB 324 RVNNAARRVHIAN-----END-----IDCKIDY-ETSKD-NRYKQAMIVRLAS 364  
 QY 480 D--LCVREVORENIF-IMNDI-----VLDVSYPECSYLCMYKQMPKRYTGDLEINCPYG 531  
 DB 365 DVSLSFSEKQFRFLVNLNNSDSARVODVH-----OLLVESMKVAGDEL----- 411  
 QY 532 LYRLALPVNQLRDHNNNLKRTHSVSPHLEPL-----YYVLSEVHFKLKVLE 585  
 DB 412 -----ISPSIFPPDSDNNNIPKEFPSTILEYLDPLVDPAVYVFMKFAVRIQSTVQ 466  
 QY 586 LRHRQID--GFPREILSL-----IMLRYLSLF-----SYGNPDVPEICRLMNLQT 629  
 DB 467 QACGSLDYENKFMKDLISMTIPDCERVGIMRTTFRLLPKNONGNEDIRKIFSR- 521  
 QY 630 FIVQFRSDIITFADEIWEMLQRLHKLPRFYLPDCSGSVYDKGRHLDPSNLOTISLSP 669  
 DB 522 FISCFVDVIFNFAKGRIDLATHLRSAL-TFFLPD----- 555  
 QY 690 RCGTKEYVMGIONKKGISGNKDDYKSPRSGLPNNLVYLLQLEILSLISVDSLPLVI 749  
 DB 556 -----VTFVEHLEK-----FCDAIFHRM-----STDTCKDLY 585  
 QY 750 I-----SSAKAPATLKLKLERTYLSMSYLDIAELPNLEVLKIMD 792  
 DB 586 LYNLLHLMNVATKYGDLDHDKMLKYKHALKITLGNSSVF-----SNDVKQLCDW 634  
 QY 793 ACCGEEMPIYMGFRNLKLLIKISFLKFKATDNFVLERLMRS-----CKR--- 842  
 DB 635 MC-----DTAKQMLSHEEVLNLEAKNKRVLEQWLRATMLATFCKHEEV 662  
 QY 843 -----LKEIPFADHTLQLELRCPPIGSGAARIK 877  
 DB 683 ESPFASMSLEKTIIPALGNKNELOOLGELIGFAT--SIDPENCEPIKLKLTLLIOR 740  
 QY 878 EQEDLGNPNVDVRI-----SNPLKESDSSEE 904  
 DB 741 GDEVLTSTGVVTLKVIKSGQFPKTANAIFQGEOTED 778  
 RESULT 6  
 YIO9 YEAST STANDARD: PRT: 1679 AA.  
 AC P40457;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)





RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.  
 CC - FUNCTION: PLAYS ESSENTIAL ROLES IN REGULATION OF CELLULAR  
 CC METABOLISM BY CATALYSING THE SYNTHESIS OF A SECOND MESSENGER,  
 CC CAMP.  
 CC - CATALYTIC ACTIVITY: ATP = 3',5'-cyclic AMP + diphosphate.  
 CC - ENZYME REGULATION: IN CONTRAST TO YEAST CYCLASE, S.POMBE CYCLASE  
 CC IS NOT LIKELY TO BE REGULATED BY RAS PROTEINS.  
 CC - SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-3 FAMILY.  
 CC - SIMILARITY: CONTAINS 21 LEUCINE-RICH REPEATS (LRR).  
 CC - SIMILARITY: CONTAINS A PP2C-LIKE DOMAIN.  
 CC -----  
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 CC -----  
 CC EMBL; M26699; AAA35284.1; -  
 CC EMBL; M24942; AAA35301.1; -  
 CC EMBL; AL023859; CA19571.1; -  
 CC PIR; A33988; A33988.  
 CC PIR; A33539; A33539.  
 CC InterPro; IPR001054; Guanylt\_cyclase.  
 CC InterPro; IPR001611; LRR.  
 CC InterPro; IPR003592; LRR.out.  
 CC InterPro; IPR003591; LRR.tyr.  
 CC InterPro; IPR001932; PP2C\_domain.  
 CC InterPro; IPR000159; RA.  
 CC Pfam; PF00211; guanylate\_cyc; 1.  
 CC Pfam; PF00560; LRR; 15.  
 CC Pfam; PF00481; PP2C; 1.  
 CC PRINTS; PR00019; LEURICHRPT.  
 CC SMART; SM00044; CYCC; 1.  
 CC SMART; SM00370; LRR; 6.  
 CC SMART; SM00369; LRR\_TYR; 1.  
 CC SMART; SM00312; PP2C; 1.  
 CC SMART; SM00314; RA; 1.  
 CC PROSITE; PS50125; GUANYLATE CYCLASES 2; 1.  
 KM Lyase; Repeat: Leucine-rich repeat; CAMP synthesis; Magnesium.  
 FT REPEAT 385 403 LRR 1.  
 FT REPEAT 404 427 LRR 2.  
 FT REPEAT 429 451 LRR 3.  
 FT REPEAT 452 475 LRR 4.  
 FT REPEAT 476 498 LRR 5.  
 FT REPEAT 501 524 LRR 6.  
 FT REPEAT 525 547 LRR 7.  
 FT REPEAT 548 570 LRR 8.  
 FT REPEAT 572 594 LRR 9.  
 FT REPEAT 595 618 LRR 10.  
 FT REPEAT 658 681 LRR 11.  
 FT REPEAT 682 705 LRR 12.  
 FT REPEAT 728 751 LRR 13.  
 FT REPEAT 753 776 LRR 14.  
 FT REPEAT 781 805 LRR 15.  
 FT REPEAT 807 828 LRR 16.  
 FT REPEAT 829 852 LRR 17.  
 FT REPEAT 854 876 LRR 18.  
 FT REPEAT 877 899 LRR 19.  
 FT REPEAT 900 922 LRR 20.  
 FT REPEAT 928 954 LRR 21.  
 FT DOMAIN 1008 1276 PP2C-LIKE.  
 FT DOMAIN 1277 1692 CATALYTIC.  
 SQ SEQUENCE 1692 AA; 19033 MW; D137CBE8770A8655 CRC64;

Query Match 3.2%, Score 149, DB 1, Length 1692;  
 Best Local Similarity 21.0%, Pred. No. 0.31;  
 Matches 141; Conservative 88; Mismatches 197; Indels 244; Gaps 35;

Db 86 VPSKSVLFHFEPDENESLSDTGRTKSDTALAARESEKSEVPDRTRSAIGIKPKENNSS 145  
 Qy 350 PLTIYVAVGLLKSRTEEDMTAKDVKSFTYNDPDRCSRVGLSDHLTSDKICLLH 409  
 Db 146 NCALSKREAGL---RRLID-----KDRSEFDKN-----LNQSTNLT----- 178  
 Qy 410 FGIPPE---DSD---IPVKMLMRSMWAEGLKLENDLEGEVEKCLQELVDRCLVLSKR 462  
 Db 179 ---PPEPISDSDSVEVQRDSLNANNWPA-----SLEBSIH-----LPRNS 216  
 Qy 463 SRDGTIRSCVHDLIYDLGVREORENIFIMNDIVDVS-----PECS 507  
 Db 217 DDDIPASAAHILDLDRHSYDSDPWRKFLPYPSILSDSDSKAPESGTSLPTEALPKQY 276  
 Qy 508 YLCWYKMP-----FKRYTGDE---INVCPLYLALTLPVROLRDNDNNLLK 554  
 Db 277 FTTFRFAPSPISGNKKKEPFLRVYRDDRTSVFTCPG-----IQTHEVILKLA 324  
 Qy 555 RTHSVSFHEPLLYVLKSEVHFELKLVLELRHQIDGFPRETLIIMLRYSLSF----- 610  
 Db 325 R--LFLPSSANFYLL---LIOFNTERIL-----LPHRQPCIFERLLSLFGCKV 369  
 Qy 611 -----SYGNFDVPPETICRLMNLQFTIVORF-----RSDIIFAEIIV---- 647  
 Db 370 TSDEINEEDNYSVARLVFTTMDIGADVLKRFSEKKTITANLDIRSNLEVIAPKIVPAH 429  
 Qy 648 ELMQLR-----HLKLPREFLPDCCSVDRGRLHDFENLQTIYSLRPCTKREVIQION 702  
 Db 430 ELISLWNSHNLSDLPDLDFEMRCV-----KLRKRLDISN-----NRSRP----- 468  
 Qy 703 VKRLGISGNKDDYKSFDSGLPNNLVYLQLELILSLISVD--YSLLPYITISSAKAFPATLK 761  
 Db 469 -----GKP---ITALRQLEVLMNSRNDIYELDPLIFGLSR--NSLK 505  
 Qy 762 KLELR-----TILSMSTYD-----TIALPRLVLYKLMDACCCEEK 799  
 Db 506 ELINANKLFELPHSTRYLVNLTYLDISYNNFVFPILITELSQLTLNLS----- 556  
 Qy 800 HPIVWGFNRL--KLLIKYSFLKFWKATNDFPLEL--MIRSKNLKPIEPADIH 855  
 Db 557 HNLSQISKISKISGLVKIKHLIYLP-----ND---LSNRLPQETIGLKNLEITIDISYNI-- 607  
 Qy 856 LQILELRCP 865  
 Db 608 TNIASISECP 617  
 RESULT 8  
 ID MYSL\_YEAST STANDARD; PRT; 1928 AA.  
 AC P08964;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Myosin-I isoform (Type II myosin).  
 GN MYO1 OR YHR02W.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=5288C;  
 RX MEDLINE=9108308; PubMed=2263482;  
 RA Sweeney F.P., Watts F.Z., Pocklington M.J., Orr E.;  
 RL "The MYO1 gene from Saccharomyces cerevisiae: its complete nucleotide  
 RT sequence.";  
 RN Nucleic Acids Res. 18:7147-7147(1990).  
 RP [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=5288C / AB972;  
 RX MEDLINE=94378003; PubMed=8091229;  
 RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,

RA Du Z., Favella A., Fulton L., Gattung S., Geisel C., Kirsten J.,  
 RA Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,  
 RA Latreille P., Louis E.J., Macri C., Maridis E., Meneses S., Mouser L.,  
 RA Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,  
 RA Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,  
 RA Vaudin M.,  
 RT "Complete nucleotide sequence of *Saccharomyces cerevisiae* chromosome  
 VII.",  
 RL Science 265:2077-2082(1994).  
 RN [3]  
 RP SEQUENCE OF 1-760 FROM N.A.  
 RC STRAIN-5288C;  
 RX MEDLINE=8811539; PubMed=3322809;  
 RA Watts F.Z., Shields G., Orr E.,  
 RT "The yeast *MYO1* gene encoding a myosin-like protein required for cell  
 division.",  
 RL EMBO J. 6:3499-3505(1987).  
 CC -1- FUNCTION: REQUIRED FOR CELL DIVISION.  
 CC -1- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 IO DOMAIN.  
 CC -----  
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 CC -----  
 DR EMBL: X53947; CAA37894.1; -  
 DR EMBL: X06187; CAA29550.1; -  
 DR EMBL: U10399; AAB68872.1; -  
 DR PIR: S05806; S05806.  
 DR PIR: S12323; S12323.  
 DR PIR: S46773; S46773.  
 DR HSSP: P08799; 1MND.  
 DR SGD: S0001065; MYO1.  
 DR InterPro: IPR000048; IO.  
 DR InterPro: IPR001609; myosin\_head.  
 DR Pfam: PF00663; myosin\_head; 1.  
 DR PRINTS: PR00193; MYOSINHEAVY.  
 DR ProDom: PD000355; myosin\_head; 1.  
 DR SMART: SM00015; IO; 1.  
 DR SMART: SM00242; MYSC; 1.  
 DR PROSITE: PS50096; IO; 1.  
 KW Myosin; Actin-binding; ATP-binding; Coiled coil; Alkylation.  
 FT DOMAIN 1 793  
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 FT DOMAIN 856 1911  
 FT NP\_BIND 180 187  
 FT MOD\_RES 460 529  
 FT CONFLICT 703 703  
 FT CONFLICT 36 36  
 FT CONFLICT 46 46  
 FT CONFLICT 59 59  
 FT CONFLICT 86 86  
 FT CONFLICT 330 330  
 FT CONFLICT 343 343  
 FT CONFLICT 421 426  
 FT CONFLICT 515 515  
 FT CONFLICT 529 535  
 FT CONFLICT 541 541  
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 FT CONFLICT 582 582  
 FT CONFLICT 588 588  
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FT CONFLICT 896 896  
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 FT CONFLICT 906 906  
 FT CONFLICT 911 911  
 FT CONFLICT 915 930  
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 FT CONFLICT 1133 1133  
 FT CONFLICT 1144 1146  
 FT CONFLICT 1159 1168  
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 FT CONFLICT 1184 1185  
 FT CONFLICT 1188 1204  
 FT CONFLICT 1224 1224  
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 FT CONFLICT 1253 1253  
 FT CONFLICT 1311 1323  
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 FT CONFLICT 1630 1646  
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 FT CONFLICT 1754 1757  
 FT CONFLICT 1777 1777  
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 FT CONFLICT 1825 1825  
 FT CONFLICT 1882 1882  
 FT CONFLICT 1902 1904  
 FT CONFLICT 1928 1928  
 SQ SEQUENCE 1928 AA; 223634 MW; 6F54C7611F43DC9F CRC64;  
 Query Match 3.1%; Score 147; DB 1; Length 1928;  
 Best Local Similarity 21.5%; Pred. No. 0.48;  
 Matches 187; Conservative 165; Mismatches 312; Indels 204; Gaps 51;  
 QY 10 MRTIESLLTSPNOSICDREELALREKVSLE-VFVKNFPR-NNVFGEMTDFEVEV 67  
 DB 1060 MSRLQSLVTESSDPLDKRDIYIKKYDQLAFETIRNLENEIEKKKINHHKELATFSKOR 1119  
 QY 68 RE-VASAEVTIQLRTGLYVGENKSOKKARRFRSLOQVAADMDHIMKESKIDDK 126  
 DB 1120 DDAVSEHGKTTAEKTRIDTEYKS-----NYQIKKEYSNFQRE-TKEDOK 1167  
 QY 127 KOVSESLVHDESSSTNDILKVNMMVGRDDQKQLLEDTLRSYGPKVPIYGMGGIG 186  
 DB 1168 K---RNSLVESLND-----KIK-ELFARLSQELSLNQLNKRISGSVENI----- 1211  
 QY 187 KTLAKEVYND-----ESILCR-FDVH-AVATISQO-----HNKEILLGL-----LHS 228  
 DB 1212 SSTFRSTYSDDPLDKRDIYIKKYDQLAFETIRNLENEIEKKKINHHKELATFSKOR 1271  
 QY 229 TIKRMDPVKAIKGEKELADM--LQSKLRKRLIYVDIWMSEVADGYRRCPTPDNAGSR 286  
 DB 1272 SSFEDOKIK-----AQMKKLKLIDMDPSIPLDILN---EPIDNC-PDESIDNK 1319  
 QY 287 ILTTT-----RNDVACYGAVEN--PSLRMSFMD--ODESWSLFRSAFSEALPYFEET 337

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Db 1320 LMLEVDYLKQDLIEATRAHYDAENALSHSKFRKIQGE-----SSLSDDSYIKLKFEFA 1373
QY 338 VG---KQIADDECHGLPL---TIVYVAGLILSKRTIEDMTAKDKV-----SFVTNDPD 385
Db 1374 SEERYKSLDEKDLTKMLPDRITMLPVGDIIKNDISIKYEERIRYKYLENYKLOEILNESN 1433
QY 386 EERCSTRLGSDYHLSLSDTKLHRCIFPEDSDIP---VKNILMRMAEGFLKLEN--- 438
Db 1434 GKLISQ---LTLDLROSKSEALLSEDLRLQDLDESTEROKELISSTIQOQOQFENCMD 1490
QY 439 DLGG-----EVEKQLQELVDRCVLVSKRSRSGTKIRSCXVHLLYDLCVREVQRE 489
Db 1491 DLQGNELRLREHIALKQAEEDVKNMASTIEK-----LTKQMKQCKELIWE---REMERH 1542
QY 490 NIFIMNDIYLDVSYPCSTLCMKQKPKRYVGEDEINCPYGLY---RALLTPVAKOR 545
Db 1543 D---SDMQLQETLLE---LKRVDYVKILSDLAHLKERLSAVEDSQQYTDEINRLK 1593
QY 546 DHNNNL-----LKRTHSVSFHLE-----PLYVYLKSEVHFKLLKVLRLRHQID 592
Db 1594 EELNCSLKAETMLKKEFALTKKLETSTNDESAKISDLK-QLDHY--TKVEMLNNE--- 1648
QY 593 GEPREILST---IMLRYSLSFGNFVDPPEICRLMNLQTFIVQFRSDIIFAEIWE 648
Db 1649 ---KDAISLAEKELYOKYKAL---NTECESLKGKIVSL-TRIKQELIESDL---NQKTD 1696
QY 649 LMQLRLHLKPRFVLPDPCSGSYDCKGRHLDPSNLQTSYLSPPRCRPEVIMGION----- 702
Db 1697 ALQISNAL-----SSSTQKNEI---TEKIKYLE---TLQLOME-QNSNGEEL 1739
QY 703 VKRLGISGNKDDYKFSRDSGLPNNLVYLOQLLELISVDSLLPVISSAKAFPAATLK 762
Db 1740 VKTLQASCN--GYKQKFEDEKQKNDIYENQTLQKLTNDLQ-----QLKN 1784
QY 763 L--KIERTYLSMSYDITAEIPNLEVLK 788
Db 1785 LHERLSDTTEKNAMLSKIHLENNVSL 1812

RESULT 9
Y511_RICPR STANDARD: PRT: 950 AA.
AC Q92D36;
DT 30-MAY-2000 (rel. 39, Created)
DT 30-MAY-2000 (rel. 39, Last sequence update)
DT 16-OCT-2001 (rel. 40, Last annotation update)
DE Hypothetical protein RP511.
GN RP511.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiidae; Rickettsia.
OX NCBI_Taxid=782;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MADRID E;
RX MEDLINE=99039499; PubMed=9823893;
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sichteritz-Ponten T., Alemark U.C.M., Podowski R.M., Neeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria."
RL Nature 396:133-140(1998).
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CC -----
DR EMBL: AJ235272; CAA14963.1.
DR InterPro: IPR001646; Pentapeptide.

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DR Pfam: PF00805; Pentapeptide: 1.
KW Hypothetical protein: Complete proteome.
SQ SEQUENCE 950 AA, 108612 MW, C047F8BC063F715 CRC64;

Query Match 3.1%; Score 145.5; DB 1; Length 950;
Best local similarity 18.2%; Pred. No. 0.23;
Matches 179; Conservative 172; Mismatches 309; Indels 321; Gaps 46;

QY 1 MAHASVASIMRTIESLTLTNSPMQSLSCDHREL-----CALREKVS 42
Db 64 LAKSNMIVYDPEFOKSLNPSIWEFLKRSDDLPRIGRIILAKAGREFODKSALDE-- 121
QY 43 SLEVFVKNFKNVNFEGEMTDFEVEYREVASAEYTIQLRTGLVGENKSQKKARRRR 102
Db 122 GLKILKECFKNEKYLKLDIAEVQ-----ERTMKNVTSLIDMLVTDK-----NQ 171
QY 103 QSLQVAEDMDHIWKSESTKIDQKGVSKESLVHDFSSTNDILKYNMVGDRDQKOL 162
Db 172 KFEFKSKDITHYIRSG-----ATEILPSDYMKSFDDIL-----QKPEKKTL 213
QY 163 LEDLTSYSGEKVPIPIVGMGIGKTTLAKEVYNDSEIICRPDVHAMATISQOHKKEIL 222
Db 214 L---KIFNTHPDV-----KQELVNNI--NNPNILKFF-----NKLFTYQETM 250
QY 223 IGLHSTIKMDRVRKMGIAELADMLQSLKR-KRYLIYLDIWSG-----EYWDGV 273
Db 251 LNSFLKEV-----AQSKPFLQEHFESKIDLKILDIIPTLNKPDKELFDL 300
QY 274 RCFPTEDNAGSRILLTTRNDEVACYAVENF-----SLRSMFMDDES-WSLEFS 323
Db 301 ---NAPKGVMSISLEKALEMAGDOLKSFPAANKTILPNNALGILINTFSVOSTYNE 355
QY 324 AAFSSALPYEFETVQK-QIADDECHGLPLTIYVAGLILSKRTIEDMTAKDKVSYFN 382
Db 356 YNPDQMLVIYGEWSKPELAHE-----IILADLNG--DYSLTGNIISIT-N 400
QY 383 DDERCSRVL-----GLSYDHLTSDLTCLLHFGIFPDSDDIPVKNLSRMAEGFLKL 436
Db 401 DPSFKLDILVEQSKGL-FDNLIN-----GVLEBD--IKN----- 433
QY 437 ENDLSEVEKCLQELVDRCVLVSKRSRSGTKIRSCXVHLLYDLCVREVQREINIMND 496
Db 434 ---SQTIKQILNMGAGVTKL--TKIPILLD----- 463
QY 497 IYLDVSYPCSTLCMKQKPKRYVGEDEI--NYCPGLYRALLTPVNRLOHNNN--- 551
Db 464 ---KPSLSKKVFPRDFIKGNTTKTKTKELISLTKNPKIKETLNNRRI 507
QY 552 ---LKRRT---HSVFSFHLPLLYVLKSEVNH---FKLKVLELRH----- 588
Db 508 FASILDKTLMDIPGINNLDKQELYNILPSMLNHPDELKIVIEVEKSHGAVSAIYNLA 567
QY 589 RQIDGPPREILSLIMLRYSLSFGNFVDPPEICRLMNLQTFIVQFRSDIIFAEIWE 648
Db 568 KRTNFEQGLPNLIKAGFNSGENYATEKVK-----DVSSSSDFEKDYI--DEIT 616
QY 649 LMQLRLHLKPRFVLPDPCSGSYDCKGR--HDFSNNLQTSYLSPPRCTKEVINGIQVKKL 706
Db 617 RKLHDKIQNGKRL---EGAILLGSLNIDFSG-----VSLKADLT 655
QY 707 GISGNKD-DYKSEFR--DSGLPNNLVYLOQLLELISVDSLLPVISSAKAFPAATLKL 763
Db 656 KYSLSKDCNFKNTNLVDATLPNLIMF--TDYNLDKAIPTLAPRLIKAQA----- 705
QY 764 KIERTYLSMSYDITAEIPNLEVLKLMADACCGEENHPVIMGFNRLKLLIKYSLFKWK 823
Db 706 KLVADKIDVVFQVQKAE-----EKKILFSKKEFLQYQV 738
QY 824 ANDNPFVLERMINSCKLKEIPEFADITHTQLLELRECPFKGESARIQKEQEDLG 883
Db 739 -----ITLEENQTVKDYIIDKLNSFPMNVTNLE-TPKINO-----YKHTNNHV 781

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FT DOMAIN 3587 3689 COILED COIL (POTENTIAL).
FT DOMAIN 3726 3730 POLY-LEU.
FT DOMAIN 203 292 GLN-RICH.
FT DOMAIN 321 1010 GLU-RICH.
FT DOMAIN 1846 2772 GLU-RICH.
FT VASPLIC 17 28 MISSING (IN ISOFORM 2 AND ISOFORM 3).
FT VASPLIC 1637 1642 OLOEI -> LATRD (IN ISOFORM 4).
FT VASPLIC 1643 3911 MISSING (IN ISOFORM 4).
FT VASPLIC 2175 2182 MISSING (IN ISOFORM 3).
FT VASPLIC 2175 2183 SADFOVE -> Q (IN ISOFORM 6).
FT VASPLIC 2895 2907 VEGFYMCFTLC -> GSSIPELASHDAYQTRICSS
FT VASPLIC 2895 2948 (IN ISOFORM 2, ISOFORM 3 AND ISOFORM 6).
FT VASPLIC 3901 3911 MISSING (IN ISOFORM 5).
FT VASPLIC 3901 3911 STOFHAGMR -> ASLTSMQHSARPTAPLEFELSH
FT VASPLIC 3901 3911 SLG (IN ISOFORM 6).
FT VASPLIC 3901 3911 K -> Q.
FT VASPLIC 3901 3911 /FTID-VAR_010926.
FT VASPLIC 3901 3911 E -> Q (IN REF. 3).
FT VASPLIC 3901 3911 M -> I (IN REF. 3).
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FT VASPLIC 3901 3911 H -> N (IN REF. 3).
FT VASPLIC 3901 3911 K -> N (IN REF. 3).
FT VASPLIC 3901 3911 OKH -> PKP (IN REF. 1 AND 2).
FT VASPLIC 3901 3911 Q -> P (IN REF. 1 AND 2).
FT VASPLIC 3901 3911 N -> D (IN REF. 3).
FT VASPLIC 3901 3911 V -> E (IN REF. 3).
FT VASPLIC 3901 3911 R -> P (IN REF. 1 AND 2).
FT VASPLIC 3901 3911 N -> T (IN REF. 3).
FT VASPLIC 3901 3911 V -> G (IN REF. 3).
FT VASPLIC 3901 3911 MISSING (IN REF. 5).
FT VASPLIC 3901 3911 A -> P (IN REF. 3).
FT VASPLIC 3901 3911 I -> V (IN REF. 3).
FT VASPLIC 3901 3911 V -> D (IN REF. 5).
FT VASPLIC 3901 3911 EI -> HE (IN REF. 7).
FT VASPLIC 3901 3911 E -> V (IN REF. 3).
FT VASPLIC 3901 3911 L -> R (IN REF. 3).
FT VASPLIC 3901 3911 T -> N (IN REF. 8).
FT VASPLIC 3901 3911 E -> D (IN REF. 3).
FT VASPLIC 3901 3911 P -> S (IN REF. 3, 7 AND 8).
FT VASPLIC 3901 3911 Q -> H (IN REF. 3).
FT VASPLIC 3901 3911 Q -> H (IN REF. 3).
FT VASPLIC 3901 3911 ESE -> OSO (IN REF. 3).
FT VASPLIC 3901 3911 P -> A (IN REF. 3).
FT VASPLIC 3901 3911 T -> S (IN REF. 3).
FT VASPLIC 3901 3911 SEQUENCE 3911 AA; 453664 MW; 3FBICBIC819B47AA CRC64;

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QY 285 SRILTTNRNDVACYAGYENFSLRMSFMDQDESNLSFKSAARSSALPYEFTVGKOLAD 344
DB 844 LKQOQIOLNEE-----TEKORNTFSFAKN-----FEVNYOEOLE 878
QY 345 ECHGLPLTIVVAGLKLKSKRTIEDKRTAKADKVSFTVNDPDERCSRVLGSLVD-HLTS-D 402
DB 879 E-----YACLKTKADDELEDSK-----NKQELFKSKLALNELHLORIN 918
QY 403 LKTCILHGIIPPESSDIPYKNLMRSMWAGFLKLENDL-GE-VKQLOELVDRCLYL-- 458
DB 919 PTVYMKSSVPEDED-----KTFVAE-----TLEMGEVVEKDTLEMEKLEYKR 962
QY 459 -----VSKSRD-----GTRKRSKVHDLIYDCVREVO-----RENI- 491
DB 963 EKLELSORLSDSEQLOKKGHSIFLNEFYKSLKKEKEQVSLRCBDELEIINHNAENVO 1022
QY 492 -----FIMNDIV-----LDVSYPECSYLCMYKMPKRYT-GDE----- 524
DB 1023 SCDDTVSSILDDGVMTSGAGSVSKYKSGEESKIVVEDKVSFENMTVGEESKQEOLE 1082
QY 525 -INCPYGLIRALLPVRNROLRDHNNILKRTHSVPSHLEPLYYLAKSEVYHKKLV 583
DB 1083 ILDLPLSVTKESL-----RATQPSENDKLQKELN-----VLKSEQNDLRL- 1123
QY 584 LELRRQIDGFPREILSLIWLRYL-SLFSYGNFDPPEICRLMNTQTFIVQFRSDIIF 642
DB 1124 -----QMEA-ORCLSLVSTHYVOVREYEMENEDKALCSL-----KEELIF 1164
QY 643 AEE-TWELMOLRLKLPREYLPDCPSGVDRGRLHDSNLO-----TISYSPROCTKE 695
DB 1165 AOEERIKELOKHQLELQTMKTOE--TGDEKPLHLILGLKQKAVSECSYELQTLCS-- 1220
QY 696 VIMQIONKKGIGISGNKDKYKFSRDSGLPNNLVYLOOLE-----LTLISVDY 743
DB 1221 -VLGEYTPALKEVNAEDKENSVDYISENEDPELODYREYODPOENMHTLNTVTEY 1279
QY 744 SLPLVIIS-AKAPFATLKLKL-----ERTYLSWSYDIIAELPNLEVLKMDA 793
DB 1280 NKLLVLOTRLSKIMQOQDGMKLEGEENLPKEET-----EFLISHQYMNLEDDIVNKS 1335
QY 794 CGGEEMHPIWGFENRLKLLILYSLFKWKAT--NDNPFYELRLMIRSKNLEPIEF- 850
DB 1336 -----KLSSLODELKRYKLEVOLELSSISLQOQLEOTYONE 1374
QY 851 ADIH-----TLQILRECPKLGESARIQKQEDLGNPNVYRISNPKESDS 900
DB 1375 AEIHLQKRLQAVSESTVPPSL-----PVD-----SVVITSDA 1408

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RESULT 11
YY08_METJA
ID YY08_METJA STANDARD: PRT: 1064 AA.
AC Q60307;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJC808.
GN MJC808.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kervilave A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weisslock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uitterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

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RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,  
 RA Klek H.-P., Fraser C.M., Smith H.O., Moese C.R., Venter J.C.;  
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus  
 RT jannaschii";  
 RT Science 273:1058-1073(1996).  
 CC -1- SIMILARITY: LOW IN THE N-TERMINAL, TO T. MARITIMA RNA POLYMERASE  
 CC BETA CHAIN.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: L77119; AAC37066.1; -  
 CC TRIGR; MJECS08; -  
 DR Hypothetical protein; Complete proteome.  
 KW SEQUENCE 1064 AA; 125624 MW; 3f57BCFC0ACEA82 CRC64;  
 SQ

Query Match 2.9%; Score 139; DB 1; Length 1064;  
 Best Local Similarity 19.6%; Pred. No. 0.67; Indels 296; Gaps 48;  
 Matches 193; Conservative 138; Mismatches 356;  
 QY 48 VKNEKNNV-----EGKTDVEVEVEVAEAETIQLRTGLTVGENKSOKKARRRQ 103  
 DB 9 INNIONNNVLEYTINELNINQPEVLEVAIK--LLNIRYDPNTIKELDEHNKN-- 59  
 QY 104 SLQQAEDMDHMKES-TKIQDKGKOVSKESLVHDSSTNDILAKVNNVAGRDQKOL 162  
 DB 60 -----TEILGNIMFLSINKPLKEROL-----LLKYLMEIGALPTDKL 99  
 QY 163 --LEDLRSYS-----BPK--VPIVGMG-----IGTKTLAKERYND 197  
 DB 100 YREDAITSLGWSFWEIPEVYLVKAKGEMLHOQNDIKIGELVEGFTLHOQNN 159  
 QY 198 ESILCREVDHAWATISOHNKKEILLGLHS--TIKMDRVKMIAGEALDMLQSKLR 254  
 DB 160 DFTMLHCGGEFTALHOQNDFTMLHQLHNIDNSMIEDLCNKIGER--ANTLKSKSKN 217  
 QY 255 KRYLIIVD-----TSCVWGVRCRFPEDNAGSRILLT--TNDVACAGVENE 305  
 DB 218 -----DDCKTKAKITITLTFEGMR--FDEEMKAIEQLIGESTKOHILKITYKOLEWI 268  
 QY 306 SLRMSFMDQESWELFKSAFSEALPYEFETVKGQIADCHGLPLTVVA----- 357  
 DB 269 DIRKNPEDYRKIY-----LTKYFEDIKILDEX--LPKAFQEAERAKSEFME 316  
 QY 358 GLKKS-KRTIEDWKT-----VAKDVAFVTNDPDEKCSRYLGSLY 396  
 DB 317 DLKSKLKFTIEERLTPGFEFDINEVDRLAKGERIVGAFYFSLLENEYEALIMYKYY 376  
 QY 397 DHLTSDTKTCLLHGIFPEDDIPVKNLMRS-----WMAEGLKLENDL--EGEVEKLO 449  
 DB 377 EK-----YFOKPLENITIGLEILRSRTIMTKAKMGGERNKLCVREGDIAGI 426  
 QY 450 ELVDR-----CLVLSKRSRDGTIKRSCKVHDLIYDLQVREVENIFIMNDIVDVS 502  
 DB 427 HKRKRPLIRRYVCIIDLOKNGNKG-----CNCEVRIKLEPENSDYKIK 471  
 QY 503 YPECSYLQMTQOPKRYTGDEIN-----YCYGLXKALLTPVN 541  
 DB 472 CPEGGRDIKYESLFKEDGEPILKENDLTALIQLEKTEDEVRYRLPY-----TPEI 524  
 QY 542 ROLGDHNNNLKRTSHVSFHLBPLYLVKSEVHFILVLVLELRHROIQDGFREILSL 601  
 DB 525 NNLRDVEIVGLIKTNH-----KGEYII--EGLSINPQITINNY--DAFVAKVKN- 570  
 QY 602 IWLRLSLFSYGNEDVPEICLMMN-----LQTFYQRRSDIITIAELWEIMQJLRH 654  
 DB 571 --AGYSNALDYIKDRVEYKAIIDKEGKNPTIDTLT-----LETLASHIYWDKNRDGH 624

QY 655 LKIPRYLPDCP--SGVDKGRHLDPSNLQITISLSPRCCKE--VIMGIONVKL-GISG 710  
 DB 625 LKPEIT--DCLPFGSYGQKSL-----TIEPLAKHNTTEMIRVDMNIENTLGLVI 675  
 QY 711 NKRDYKSFRRSGLP---NNLVYLOQ--LEILSLISVDYSLPVIISAKAPATLKKLLE 766  
 DB 676 SRDNKIFKKGIIIPMHNRRPIFIEAMDITLRGNDIDL--KSGK-----TSGIKRE 727  
 QY 767 RYLSMSYLDI-----IADLPNEVLKLDMDACCGEEMHPYMGFNRLKLLIKYFLK 821  
 DB 728 REGVNIPMIGVSWIGVGNIKIDIMELW-----EIVH--LKGFEFKKAMINYEAKKL 779  
 QY 822 WK-----ATQDNFVYLERLMIRSCNKL--EIIPEF-- 850  
 DB 780 LKHDDYDRNEADRRAKKIVNNILGANPOLNASEWLSKILDFTLKLNKGMDRIPLIYL 839  
 QY 851 -----ADIHTQLIETRE 863  
 DB 840 KPYTNEDMKELKHTYKVKRLRE 862

RESULT 12  
 CUT1\_SCHPO STANDARD; PRT; 1828 AA.  
 ID CUT1\_SCHPO  
 AC P18296; 094304;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Separin (EC 3.4.22.-).  
 GN CUT1 OR SPCC5E4.04.  
 OS Schizosaccharomyces pombe (fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetaceae; Schizosaccharomycetaceae;  
 OC NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RX MEDLINE=90367123; PubMed=2203537;  
 RA Urawa S., Samejima I., Hirano T., Tanaka K., Yanagida M.;  
 RT "The fission yeast cut1+ gene regulates spindle pole body duplication  
 RL Cell 62:913-925(1990).  
 RN [2]  
 RP REVISIONS.  
 RC STRAIN=972;  
 RX MEDLINE=97133291; PubMed=8978688;  
 RA Funabiki H., Kumada K., Yanagida M.;  
 RT "Fission yeast Cut1 and Cut2 are essential for sister chromatid  
 RT separation, concentrate along the metaphase spindle and form large  
 RL complexes";  
 RL EMBO J. 15:6617-6628(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RX Wood V., Rajandream M.A., Barrell B.G., Rieger M.;  
 RT Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
 RL -1- FUNCTION: ESSENTIAL FOR CHROMOSOME DISJUNCTION, REGULATES SPINDLE  
 CC POLE BODY DUPLICATION.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C50.  
 CC -----  
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 CC -----  
 CC EMBL: M36179; AAB06192.1; -  
 DR EMBL; AL033406; CAA21959.1; -

QY	10	MRTIESLTFNSMO-----SLSCDHREELCALRENVSLFEYVFNFEKNVGE	53
Db	234	LATINNIQSODGPFOWIERSPFSSQVQLANSREITLARILTFRSMIO-----NNA---	28
QY	60	MTDEVEVEEVAASAEYTTIOLRLTGTVGENKS--OKKARRRFSSIOQY-----AEDM	11
Db	283	LOSQFLILISIA-----LMLNILLSQKADKEDVDVQLETRILQLEFSKVOLCKSEDE	33
QY	114	H--IMKESRKIDQKQVKSBLVH-----DESSSTNDI-L	14
Db	337	GSILNKDMQTLHHLEENLSEKESRHLIOLLSQLYKYNDEQLSAAYIRGYSLSFEDISF	39
QY	147	KVK-----NNWGRDQKQLELFTRSYSGEPKVPYIVMGSIGT	18
Db	397	KLKFLLFSRLSIHNSICFPENLIQELISSIQLFYNALPYBALHLDT-----	44
QY	189	TLAKEYNDESLICRFDVHAMATTSOQHKKELLGLHSTIKMDRVKMGIEALADL	24
Db	449	ERSFRLFNDSIV--FDDTVPAL-----NISELWITLSSVVR-----DIVEDEL--L	49
QY	249	QKSIKRRLLIYLDIINSCFVWDGVRCPFIEDNAGSRILLTTRNDEVACYAGVENFSIR	30
Db	493	NIQLKRFKLMFTPHI-----IRSFSEL	51
QY	309	MSFMQDESM--SLFKAASFSEALPYEFYVGK---QIADCHGLPLTIVYAGLL	36
Db	516	TKRQSSLEBCNLAAVYEDAEFPQKLSNHLNLCYKSSNNVYARCEIISIKIAY-----	57
QY	361	KSKRTIEDMKYVAKDYKSEFVTDNDP---ERCSRVLGSIYDHLTSDLTKTCLHFGIPE	41
Db	571	SHKLTNDEYTLIKLKLNQLEHRDHSIQLQEKCD-VLHTFQND-----LYGTTSV	62
QY	416	DSIDIPKMLMRSMAGELKLENDLEBEYKCOQLVDRLVYKSRSDGTRISKYH	47
Db	622	GKSSVLDNLK---RLPNSLTJSDNISEIKLESTISYSLKLFECAGNEGRYANASA-	67
QY	476	DLIYDLCVREYQRENIFIMNDIV-----DVSYPECSYLCAMKMPFRFVYGEIN	52
Db	677	LSFKLSLMLHEKEVLLKTNVSCVLANGYNDIKFEE-MVLCYIK-----GDO--	72
QY	527	YCPYGLYALLTPVNRQROHDNNNLKPRHVSFSLHEPLYYVYKSEVYHFKLLVLEL	58
Db	725	-----NLEENSNNNAK-----LAINESILCSWENILCY	75
QY	587	RHRQIDGPREILSLI--WLRYSLSF-----SYGNPDVPEI---CRLMNQITFYQ	63
Db	754	RAREEDS---RLITLIESWILFISRBSSVYSRCSFIDFELINSILNFPFCFHTVPSGKL	81
QY	634	RFRSDIIFAEIWMQ-LRHLKLPF-----YL	66
Db	811	TFE--LAFLEIFELNCLLHQLFSKYVLIITGLTSLDKYMTLGPSCGAHLEFYTKCYSL	86
QY	663	PDCRSGSVDRKHLDESNLOTISYLSBRCCTKEVINGIONVAKKLGISGNKDDYKSPRDSG	72
Db	868	ROCKSS-----PFINFNWVSYKYLILITGNTDKGILOTKYSLSEED-----FNSNG	91
QY	723	LPN-----NLVYLOQLEIL-SLISVDSL--LPVITSSAKAPATLKLKLER-----TYLS	77

```

Db      916 LSTSVS:NTLLYR:QI:SDALFQLGTTVTSVIGFTIMQNLKVIKIGLFSSSNEHNGCKYIT 975
QY      772 WSYLDIIA 779
       1  : 1
Db      976 WRLEPAVA 983

RESULT 13
DYHC YEAST
ID      DYHC_YEAST      STANDARD:      PRT: 4092 AA.
AC      P36022;
DT      01-JUN-1994 (Rel. 29, Created)
DT      01-JUN-1994 (Rel. 29, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      Dynein heavy chain, cytosolic (DYHC).
GN      DYN1 OR DHC1 OR YKR054C.
OS      Saccharomyces cerevisiae (Baker's yeast).
OC      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC      Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX      NCBI_TaxID=4932;
       [1]
RN      RP      SEQUENCE FROM N.A.
RX      MEDLINE=94068566; PubMed=8248224;
RA      Eshel D., Urrestarazu L.A., Vissers S., Jauniaux J.-C.,
RA      van Vleet-Reedijk J.C., Planta R.J., Gibbons I.R.;
RT      "Cytoplasmic dynein is required for normal nuclear segregation in
RT      yeast.";
RN      RL      Proc. Natl. Acad. Sci. U.S.A. 90:11172-11176(1993).
       [2]
RN      RP      SEQUENCE FROM N.A.
RX      Vissers S., Urrestarazu L.A., Jauniaux J.-C.;
RN      Submitted (MAR-1994) to the EMBL/Genbank/DBJ databases.
       [3]
RN      RP      SEQUENCE OF I-3457 FROM N.A.
RX      MEDLINE=94052110; PubMed=8234262;
RA      Li Y.-Y., Yeh E.-Y., Hays T., Bloom K.S.;
RT      Proc. Natl. Acad. Sci. U.S.A. 90:10096-10100(1993).
       [4]
RN      RL      "Disruption of mitotic spindle orientation in a yeast dynein mutant.";
RX      Proc. Natl. Acad. Sci. U.S.A. 90:10096-10100(1993).
       [5]
RN      RP      -1- FUNCTION: DYNEIN HAS ATPASE ACTIVITY. CYTOPLASMIC DYNEIN ACTS AS A
RX      MOTOR FOR THE INTRACELLULAR RETROGRADE MOTILITY OF VESICLES AND
RX      ORANELLAS ALONG MICROTUBULES. REQUIRED TO MAINTAIN UNIFORM
RX      NUCLEAR DISTRIBUTION IN HYPHAE. MAY PLAY AN IMPORTANT ROLE IN THE
RX      PROPER ORIENTATION OF THE MITOTIC SPINDLE INTO THE BUDDING
RX      DAUGHTER CELL YEAST. PROBABLY REQUIRED FOR NORMAL PROGRESSION OF
RX      THE CELL CYCLE.
RN      RL      -1- SUBUNIT: CONSISTS OF AT LEAST TWO HEAVY CHAINS AND A NUMBER OF
RX      INTERMEDIATE AND LIGHT CHAINS.
RN      RL      -1- SUBCELLULAR LOCATION: CYTOPLASMIC. PROBABLY BINDS INDIRECTLY TO
RX      THE INNER PLASMA MEMBRANE.
RN      RL      -1- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
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CC      or send an email to license@isb-sib.ch).
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CC      CC
DR      EMBL; Z21877; CAA79923.1; -
DR      EMBL; L15626; AAL16055.1; -
DR      EMBL; Z28279; CAA82132.1; -
DR      PIR; S38128; S38128.
DR      HSSP; P56255; 1PJR.
DR      SDD; S0001762; DYN1.
DR      InterPro; IPR004273; Dynein_heavy.
DR      Pfam; PF03028; Dynein_heavy; 1.
DR      Motor protein; Microtubules; Dynein; ATP-binding; Coiled coil;
DR      Karyogamy.
KM      Karyogamy.
FT      DOMAIN 154 175 COILED COIL (POTENTIAL).
FT      DOMAIN 486 508 COILED COIL (POTENTIAL).
FT      DOMAIN 542 566 COILED COIL (POTENTIAL).
FT      DOMAIN 932 959 COILED COIL (POTENTIAL).

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FT DOMAIN 1042 1063 COILED COIL (POTENTIAL).
FT DOMAIN 1681 1705 COILED COIL (POTENTIAL).
FT DOMAIN 1894 1922 MICROTUBULE-BINDING (POTENTIAL).
FT DOMAIN 2993 3092 COILED COIL (POTENTIAL).
FT DOMAIN 3242 3300 COILED COIL (POTENTIAL).
FT DOMAIN 3532 3608 COILED COIL (POTENTIAL).
FT NP_BIND 1796 1803 ATP (POTENTIAL).
FT NP_BIND 2074 2081 ATP (POTENTIAL).
FT NP_BIND 2418 2425 ATP (POTENTIAL).
FT NP_BIND 2760 2767 ATP (POTENTIAL).
FT CONFLICT 589 589 Y -> C (IN REF. 3).
FT CONFLICT 601 601 V -> A (IN REF. 3).
FT CONFLICT 1364 1364 E -> A (IN REF. 3).
FT CONFLICT 2118 2119 ML -> IV (IN REF. 1).
SQ SEQUENCE 4092 AA: 471337 MW: 309DF447E8E2D6B CRC64;

Query Match 2.9%; Score 138.5; DB 1; Length 4092;
Best Local Similarity 18.2%; Pred. No. 4.3; Indels 319; Gaps 44;
Matches 168; Conservative 148; Mismatches 289;

QY 32 EELCALREKVSLEVEKFEKNVGEKMTDFEVEVEVAASAEYITQRLTGTGVEGNK 91
DB 1051 EDNRDREAVEEDMDINTSLKNTVITIEAVN--VNKRHL--TERDIQIKLGSVMRAL 1105
QY 92 SOKKARRR-----KSLQOYAEKMDHIMKSTKIDKQKQVSKESL----- 134
DB 1106 KIKVREPEHVVYIDOLDNDFESSLSRSLSYEOL-----OKHRVYIAKSEEGV 1154
QY 135 --VHDSSSTNDILKYNKNNVGRDORCOLLELTRSYSGEPKVPYIVGSGIGKTTAK 192
DB 1155 ENINNLISQINSEWSV-----RKPISPILT-----PPRAKIL----- 1187
QY 193 EYVNDSEILCRFDVHAMATISQOHKKEILLGLHSTIKMDRVMKIGAEALDMLQKSL 252
DB 1188 EEFNEISITKIKKMHSAVAAAKK-----LLIPVLMQDLTHVEEYKTYDLVWRSI 1238
QY 253 KRRRYLIVDDIMSCVWQVRCFPEEDNAGSRILITTNDEVACVAGVENSLSRSEM 312
DB 1239 K-----NIMEVORTFEPR-----WCWVDVLLQLQSDIANFLRADEL 1275
QY 313 DQD-ESMSLEKSAFSESEALPYEFETVGRQIADCHGLPLTVIVVAGLSKSKRTIEDMK 371
DB 1276 PRAVKQFEMWKS-LFSQVNNLTGVNKKIIVBLKD-----GALKPRH-----WNM 1317
QY 372 VAKDV--KSFVNDPDE--RCSRVLGISTYH--LTSDLKTCLLHFGIFPEDSDIPVK 422
DB 1318 IFRDICKRQIQKMLDKLEFSLKDVAVMLTNEILITKTIIRAQKEFYI-----EKSLN 1372
QY 423 NLMRSMABEG-----LKLEND--LEGEVEKCLQELVDR-----CLAVY 459
DB 1373 RIKKFKKQAYEVIEHSSGLKLVREWDVLEQACKEDLEELVSKMASNYKIFEDQCLDLE 1432
QY 460 SKRSRDTKIRSKVDL--IYDLCEVRORENIFIMNDIVDVSYPECSYICMYKMP 516
DB 1433 SKL-----TKISEIQVWVVEQFYWLDLYGLGENLDIQNLPLETS-----K 1475
QY 517 FKVYTGDEINPCYGLYRALLTFVNRQLRDHNNMLKRTHSVFSHLEPLYLVLSSEV 576
DB 1476 FKSLTSE-----YKMTT-----RAFQDLTTIEVHIHPEDTTLKLTID 1514
QY 577 HFKLLK-----VLELHRQIDGPRRELISLIMLRYSLSFYGVNDVPELCRLMNQTFI 631
DB 1515 SLKMIKSSSTLEFKORQ--FPR-----FYFLGNDL----- 1545
QY 632 VQFRSDIILFAEIEIMQLRLKLPFYLPDCPSGVYDKGRHL-----ESNLQ 682
DB 1546 -----LKI-----IGSGKHQVSKFMKMKMGSTIE 1570
QY 683 TISYLSPPCCTKEVINGIONVKKLGISGNKDYKSFSDSGLPNNLVYLOQLLEISLSDV 742
DB 1571 STFL-----EDFITGVNSVE--GEVLNMLNEKIELEKDS-----IQAGEWMLNIDTE 1614

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QY 743 YSLPVIITSSAKAPATPKKIKLEERTLSMSYIDILNLEPNLEVKIMDDACGSEMHPI 802
DB 1615 IKL-----SVFTQRODLGOLK-----DGLDEVVSKTIFQAILLSAQ----- 1653
QY 803 VMGFNRLLKILKYSEFKKATNDNPNVLERLIMRSCKMLKE-----IPLEFADITHLQL 858
DB 1654 VMTEELVEKCLQTNQFQSKYKEVDMKIKGLDLKNSDVNKKIEALIVEY--LHNNV 1711
QY 859 I-ELRECPPLGESA-----ARIQK 877
DB 1712 IGLKNCSTK--EEARLMAKVK 1733

RESULT 14
CENE_HUMAN STANDARD; PRT; 2663 AA.
ID CENE_HUMAN
AC 002224;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Centromeric protein E (CENP-E protein).
GN CENPE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93024922; Pubmed=1406971;
RA Yen T.J., Li G., Schaar B.T., Szilak I., Cleveland D.W.;
RT "CENP-E is a putative kinetochore motor that accumulates just before
RT mitosis.";
RL Nature 359:536-539(1992).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=95196755; Pubmed=7889940;
RA Thresher D.A., Jordan M.A., Schaar B.T., Yen T.J., Wilson L.;
RT "Mitotic HeLa cells contain a CENP-E-associated minus end-directed
RT microtubule motor.";
RL EMBO J. 14:918-926(1995).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=98437347; Pubmed=9763420;
RA Chan G.K.T., Schaar B.T., Yen T.J.;
RT "Characterization of the kinetochore binding domain of CENP-E reveals
RT interactions with the kinetochore proteins CENP-F and hBUBR1.";
RL J. Cell Biol. 143:49-63(1998).
CC -1- FUNCTION: MINUS-END DIRECTED MICROTUBULE MOTOR. PROBABLE
CC KINETOCHORE MOTOR. ACCUMULATES JUST BEFORE MITOSIS AT THE G2 PHASE
CC OF THE CELL CYCLE. PROBABLY IMPORTANT FOR CHROMOSOME MOVEMENT
CC AND/OR SPINDLE ELONGATION.
CC -1- SUBUNIT: INTERACTS WITH CENP-F AND BUBR1 KINASE.
CC -1- SUBCELLULAR LOCATION: ASSOCIATES WITH KINETOCHORES DURING
CC CONGSSION, RELOCATES TO THE SPINDLE MIDZONE AT ANAPHASE, AND IS
CC QUANTITATIVELY DISCARDED AT THE END OF THE CELL DIVISION.
CC -1- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: 215005; CAA78727.1; -.
CC PIR: S28261; S28261.
CC HSSP: P37119; 3KAR.
CC MTM: 117143; -.
CC InterPro: IPR001752; kinesin.
CC Pfam: PF00225; kinesin; 1.
CC PRINTS: PR00380; KINESINHEAVY.
CC SMART: SM00129; KISC; 1.

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DR SMART; SM00369; LRR\_TYP: 2.

DR SMART; SM00255; TIR: 1.

DR PROSITE; PS50104; TIR: 1.

KW Receptor; Immune response; Inflammatory response; Signal;

KM Transmembrane; Repeat; Leucine-rich repeat; Glycoprotein.

FT SIGNAL 1 21

FT CHAIN 22 904

FT DOMAIN 22 704

FT TRANSMEM 705 725

FT DOMAIN 726 904

FT REPEAT 50 73

FT REPEAT 75 97

FT REPEAT 98 121

FT REPEAT 123 145

FT REPEAT 147 169

FT REPEAT 170 193

FT REPEAT 196 219

FT REPEAT 247 270

FT REPEAT 273 296

FT REPEAT 298 320

FT REPEAT 354 377

FT REPEAT 379 403

FT REPEAT 406 429

FT REPEAT 431 454

FT REPEAT 455 478

FT REPEAT 505 528

FT REPEAT 530 552

FT REPEAT 561 584

FT REPEAT 586 608

FT REPEAT 610 632

FT REPEAT 634 659

FT DOMAIN 754 896

FT CARBOHYD 52 52

FT CARBOHYD 57 57

FT CARBOHYD 70 70

FT CARBOHYD 124 124

FT CARBOHYD 166 196

FT CARBOHYD 247 247

FT CARBOHYD 252 252

FT CARBOHYD 265 265

FT CARBOHYD 275 275

FT CARBOHYD 291 291

FT CARBOHYD 398 398

FT CARBOHYD 413 413

FT CARBOHYD 507 507

FT CARBOHYD 636 636

FT CARBOHYD 662 662

SQ SEQUENCE 904 AA: 103828 MM: 034E05ECA7AAD2F7 CRC64;

Query Match 2.9%; Score 135; DB 1; Length 904;

Best Local Similarity 23.8%; Pred. No. 0.93;

Matches 67; Conservative 48; Mismatches 111; Indels 56; Gaps 13;

QY 599 LSLIMRLVSL-PSYGNFVPPPEICRLM--NLQTFIVQRKSDIIFAEIWMQLMQLRL 655

DB 269 LGLKWTNLMLDLSYNNLVGNDSPAWLPQLVFFLE-YNNIQHLFSLHGLFNVRYL 327

QY 656 KLPFLPLDPCS-GSVDKGRHLDFSNIQTSYSPR-----CCTKEYIMGIQVKKLGIS 709

DB 328 NLKRSTKQSTIASLPKIDDFQWLKCLEHNMEDNDIPGKSNMFTGLINLKLYSTLS 387

QY 710 GNRDYSKSPFSDGLPNNLVYLOQLLSLSVSYSLPVIISAKAFPAATLKL-KLERT 768

DB 388 -----NSFTSLRTLTNETFEVSLAHSPLHL-----NLTKNKISKIESD 425

QY 769 YLSWSYLDITIAELPNEVYKL---MDDACCGEWHPIYGFNRKILLIKYSFLKFWKA 824

DB 426 AFSW-----LGHLEVDLGLNEIGQELTGQEWKLENIFE-----IYLSYKRYLQL 471

QY 825 TNDNF---PYLERLMIR--SCKNLKEIPLEFADIHITLQLEL 861

DB 472 TRNSFALVPSLQRLMLRVALKNVDSPPSPQPLRNLTJIDL 513

Search completed: September 12, 2002, 14:08:19  
Job time: 577 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 12, 2002, 13:57:37 ; Search time 80.61 Seconds  
(without alignments)  
1942.196 Million cell updates/sec

Title: US-09-864-680-3

Perfect score: 4712

Sequence: 1 MAHASVASLMRTIESLTLTFN.....PVDYRISNPKESDSDSEEH 905

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

1: SP\_ARCHAEA:\*  
2: SP\_BACTERIA:\*  
3: SP\_FUNGI:\*  
4: SP\_HUMAN:\*  
5: SP\_INVERTEBRATE:\*  
6: SP\_MAMMAL:\*  
7: SP\_MHC:\*  
8: SP\_ORGANELLE:\*  
9: SP\_PHAGE:\*  
10: SP\_PLANT:\*  
11: SP RODENT:\*  
12: SP\_VIRUS:\*  
13: SP\_VERTEBRATE:\*  
14: SP\_UNCLASSIFIED:\*  
15: SP\_RVIRUS:\*  
16: SP\_BACTERIAP:\*  
17: SP\_ARCHAEP:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4712	100.0	905	09SNW0	09SNW0 capsicum ch
2	1257.5	26.7	933	09LKO0	09LKO0 solanum tub
3	1245	26.4	938	09SM52	09SM52 solanum aca
4	1242.5	26.4	912	09S704	09S704 solanum tub
5	1234.5	26.2	937	09XGF5	09XGF5 solanum tub
6	980	20.8	1824	09LJL4	09LJL4 lycopersico
7	980	20.8	1824	09A485	09A485 lycopersico
8	970	20.6	1825	09LJL0	09LJL0 lycopersico
9	901	19.1	1245	09A109	09A109 lycopersico
10	875.5	18.6	1245	09A109	09A109 lycopersico
11	864	18.3	1241	09A105	09A105 lycopersico
12	852.5	18.1	1255	09A106	09A106 lycopersico
13	849.5	18.0	1271	09A107	09A107 lycopersico
14	848.5	18.0	1263	09A106	09A106 lycopersico
15	834.5	17.7	1206	09SNO9	09SNO9 lycopersico
16	834.5	17.7	1257	09SBC3	09SBC3 lycopersico

17	828.5	17.6	1257	10	081137	081137 lycopersico
18	741.5	15.7	907	10	09C644	09C644 arabidopsis
19	723.5	15.4	909	10	09M5A1	09M5A1 arabidopsis
20	717	15.2	908	10	09ZSY3	09ZSY3 arabidopsis
21	717	15.2	1584	10	09MAG6	09MAG6 arabidopsis
22	716.5	15.2	908	10	09FJK8	09FJK8 arabidopsis
23	707	15.0	1049	10	09A4H3	09A4H3 arabidopsis
24	698	14.8	901	10	09FJH5	09FJH5 arabidopsis
25	696.5	14.8	831	10	09M668	09M668 arabidopsis
26	684	14.5	906	10	09ZSY4	09ZSY4 arabidopsis
27	669	14.2	1266	10	09XET3	09XET3 lycopersico
28	667	14.2	1240	10	024016	024016 lycopersico
29	666	14.1	899	10	09C646	09C646 arabidopsis
30	656.5	13.9	894	10	09AGC0	09AGC0 oryza sativ
31	653	13.9	839	10	09SX38	09SX38 arabidopsis
32	652	13.8	835	10	09SNC5	09SNC5 arabidopsis
33	651	13.8	820	10	09M667	09M667 arabidopsis
34	637.5	13.5	847	10	09STE7	09STE7 arabidopsis
35	636	13.5	906	10	09XIF0	09XIF0 arabidopsis
36	632.5	13.4	1155	10	09AHW5	09AHW5 arabidopsis
37	629.5	13.4	1297	10	0945S6	0945S6 lycopersico
38	618.5	13.1	900	10	09C645	09C645 arabidopsis
39	614.5	13.0	1220	10	024015	024015 lycopersico
40	614	13.0	821	10	004093	004093 arabidopsis
41	612.5	13.0	904	10	038834	038834 arabidopsis
42	608.5	12.9	852	10	09SVK4	09SVK4 arabidopsis
43	608.5	12.9	926	10	09ATQ3	09ATQ3 triticum ae
44	600	12.7	920	10	09ATQ8	09ATQ8 triticum ae
45	596.5	12.7	959	10	094G20	094G20 oryza sativ

## ALIGNMENTS

RESULT 1  
ID 09SNW0 PRELIMINARY; PRT; 905 AA.  
AC 09SNW0;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE DISEASE RESISTANCE PROTEIN BS2.  
GN BS2.  
OS Capsicum chacoense.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; euasterids I; Solanales; Solanaceae; Capsicum.  
OX NCBI\_TaxID-107817;  
RN [1]  
RS SEQUENCE FROM N.A.  
RX MEDLINE-20040692; PubMed-10570214;  
RA Tai T.H., Dahlbeck D., Clark E.T., Gajiwala P., Paslon R.,  
RA Whalen M.C., Stahl R.E., Staskiewicz B.J.;  
RT "Expression of the Bs2 pepper gene confers resistance to bacterial  
RT spot disease in tomato."  
RL Proc. Natl. Acad. Sci. U.S.A. 96:14153-14158(1999).  
DR EMBL: AF202179; AAF09256.1; -  
DR InterPro: IPR000767; Disease\_resist.  
DR InterPro: IPR002182; NB-ARC.  
DR Pfam: PF00931; NB-ARC.1  
DR PRINTS: PR00364; DISEASEREST.  
SQ SPROUCE 905 AA; 104459 MW; 8ED897D30E7A75B CRC64;

Query Match 100.0%; Score 4712; DB 10; Length 905;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 905; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAHASVASLMRTIESLTLTFNSPMOSLSCDHRBELCALFEKYSLFVFKNEKNVFGEM 60  
DB 1 MAHASVASLMRTIESLTLTFNSPMOSLSCDHRBELCALFEKYSLFVFKNEKNVFGEM 60  
OY 61 TDFEVEVEVSAEYITQLTLGTIVLGENSKKKARRRRFQSLQYVAEDMDHIMKEST 120

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Db      61 TDFEVEVRASAAYETIOLRLGTVLGENKSOKKARRRFRQSLQOVAEDMDHIMKES1 120
Qy      121 KIODKGOVSKESIVHDESSSTNDILKVNKNWGRDQKOLLEDTTRYSQGPXPYIPV 180
Db      121 KIODKGOVSKESIVHDESSSTNDILKVNKNWGRDQKOLLEDTTRYSQGPXPYIPV 180
Qy      181 GMGIGKTTLAKEVYNDESILCFDVAHANATISQHNKKEILLGLHSTIKMDRVMKMG 240
Db      181 GMGIGKTTLAKEVYNDESILCFDVAHANATISQHNKKEILLGLHSTIKMDRVMKMG 240
Qy      241 EAEIADMLOKSLKRRKRYLLVDDINSCVWDGVRCPPEEDNAGSRIILLTRNDEVACYA 300
Db      241 EAEIADMLOKSLKRRKRYLLVDDINSCVWDGVRCPPEEDNAGSRIILLTRNDEVACYA 300
Qy      301 GVENFSLRMSFMDODESWSLFFKSAFSSALPPEFETVKQIADDECHGLPLTIVVAGLL 360
Db      301 GVENFSLRMSFMDODESWSLFFKSAFSSALPPEFETVKQIADDECHGLPLTIVVAGLL 360
Qy      361 KSKRTIEDKTYAKDVKSVTNDPDERCSRVGLSYDHLTSDLTCTLHFGIFPEDSDIP 420
Db      361 KSKRTIEDKTYAKDVKSVTNDPDERCSRVGLSYDHLTSDLTCTLHFGIFPEDSDIP 420
Qy      421 VKNLRSMWAEGLKLENDLBEVEKCOELVDRCGLVYVSKSRDGTIKRSCKVHDLIYD 480
Db      421 VKNLRSMWAEGLKLENDLBEVEKCOELVDRCGLVYVSKSRDGTIKRSCKVHDLIYD 480
Qy      481 IGVREORENIFIMNDIVLVSYPECSYLCMKQPFKRTGDEINCYCYGALRYALLTPV 540
Db      481 IGVREORENIFIMNDIVLVSYPECSYLCMKQPFKRTGDEINCYCYGALRYALLTPV 540
Qy      541 NQOLDHONNNLKTHTSYFSPHLEPLYVYVLSKVYHFKLLVLELRHQIDGPREILS 600
Db      541 NQOLDHONNNLKTHTSYFSPHLEPLYVYVLSKVYHFKLLVLELRHQIDGPREILS 600
Qy      601 IIMLRYSLSFGYNDVPEICRLNNLOTFTYQRRSDIIFAEETIMELMOLRHLKLPRE 660
Db      601 IIMLRYSLSFGYNDVPEICRLNNLOTFTYQRRSDIIFAEETIMELMOLRHLKLPRE 660
Qy      661 YLPDPSGVKGRHLDPSNLTQITISYLSPRCTKEVINGIQNVKLGISGNDKDYKSPFD 720
Db      661 YLPDPSGVKGRHLDPSNLTQITISYLSPRCTKEVINGIQNVKLGISGNDKDYKSPFD 720
Qy      721 SGLPNLNVYLOOELTSLISVDYSLLPYITISAKAPATLKKLERYLLSYSDITIAE 780
Db      721 SGLPNLNVYLOOELTSLISVDYSLLPYITISAKAPATLKKLERYLLSYSDITIAE 780
Qy      781 LPNLEVLKMDACCGEEMHPYVMGFNRLKLLIKYSFLKFKATNDNPPYLERLMIRSC 840
Db      781 LPNLEVLKMDACCGEEMHPYVMGFNRLKLLIKYSFLKFKATNDNPPYLERLMIRSC 840
Qy      841 KNLKEIPLEFADITHLIELRECPKLGESAAARIQOEEDLGNNPVDRISNPLKESDS 900
Db      841 KNLKEIPLEFADITHLIELRECPKLGESAAARIQOEEDLGNNPVDRISNPLKESDS 900
Qy      901 DSEEH 905
Db      901 DSEEH 905

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Ox      NCBI_TaxID=4113;
Rn      [1]
Rp      SEQUENCE FROM N.A.
Ra      van der Vossen E.A.G., Rouppe van der Voort J.N.A.M., Kanyuka K.,
Ra      Bendahmane A., Sandbrink H., Baulcombe D., Bakker J., Stiekema W.J.,
Ra      Klein-Lankhorst R.M.;
Rt      "Homologs of a single resistance gene cluster of potato confer
Rt      resistance to distinct pathogens: a virus and a nematode.";
Rl      Plant J. 0:0-0(2000)
Dr      EMBL; AF26747; AF76163.1; -
Dr      InterPro; IPR000767; Disease_resist.
Dr      InterPro; IPR002182; NB-ARC.
Dr      Pfam; PF00931; NB-ARC; 1.
Dr      PRINTS; PR00364; DISEASERISIT.
Dr      NON_TER 933
Ft      SEQUENCE 933 AA, 107303 MW; A6197F92A1B9755E CRC64;

Query Match      26.7%; Score 1257.5; DB 10; Length 933;
Best Local Similarity 35.1%; Pred. No. 4.4e-76;
Matches 345; Conservative 148; Mismatches 348; Indels 141; Gaps 30;

Qy      1 MAHASVASIMRTTESLITNSPMQSLSCDREBELCALREKVSLEVFKNFEKN-NVEGE 59
Db      1 MAHASVASIMRTTESLITNSPMQSLSCDREBELCALREKVSLEVFKNFEKN-NVEGE 59
Qy      60 ---MTDFEVEVRASAAYETIOLRLGTVLGENKSOKKARRRFRQSLQOVAEDMDHIW 116
Db      60 ---MTDFEVEVRASAAYETIOLRLGTVLGENKSOKKARRRFRQSLQOVAEDMDHIW 116
Qy      48 HEGTILIKETIYEVAATTTEDWDSESNVFLAONLENSRAMETFFVLEQALECIDSTV 107
Db      48 HEGTILIKETIYEVAATTTEDWDSESNVFLAONLENSRAMETFFVLEQALECIDSTV 107
Qy      117 KESTIKODKGOVSKRE--SLVHDFSSSTNDILKVNKNWGRDQKOLLEDTTRYSQGP 174
Db      117 KESTIKODKGOVSKRE--SLVHDFSSSTNDILKVNKNWGRDQKOLLEDTTRYSQGP 174
Qy      108 KOMMAASDSMKDLKPQTSLSV--SLPEHDVOPDINIVGRENEFEMLDQALRG-GRLL 163
Db      108 KOMMAASDSMKDLKPQTSLSV--SLPEHDVOPDINIVGRENEFEMLDQALRG-GRLL 163
Qy      175 KYIPIVGMGIGKTTLAKEVYNDESILCFDVAHANATISQHNKKEILLGLHSTIKMD 234
Db      175 KYIPIVGMGIGKTTLAKEVYNDESILCFDVAHANATISQHNKKEILLGLHSTIKMD 234
Qy      164 EVAVSTVGMGIGKTTLAALVSDPYIMSRFDIRAKATVSQEVCRVAVFGILSTLSDPD 223
Db      164 EVAVSTVGMGIGKTTLAALVSDPYIMSRFDIRAKATVSQEVCRVAVFGILSTLSDPD 223
Qy      235 RYKMGAEIADMLOKSLKRRKRYLLVDDINSCVWDGVRCPPEEDNAGSRIILLTRND 294
Db      235 RYKMGAEIADMLOKSLKRRKRYLLVDDINSCVWDGVRCPPEEDNAGSRIILLTRND 294
Qy      224 -----DQLADRLOKHLKGRYLVYIDDIWTEAMDILKLCFPDPCYN-GSILLITTRV 275
Db      224 -----DQLADRLOKHLKGRYLVYIDDIWTEAMDILKLCFPDPCYN-GSILLITTRV 275
Qy      295 EVACYAGVENFSLRMSFMDODESWSLFFKSAFSS-ALPYEFETVKQIADDECHGLPLT 353
Db      295 EVACYAGVENFSLRMSFMDODESWSLFFKSAFSS-ALPYEFETVKQIADDECHGLPLT 353
Qy      276 EVAENASSGKPPHNRIMNFDESNNLHKIKIFETGYSPEFENIGQIALKCGGLPLAI 335
Db      276 EVAENASSGKPPHNRIMNFDESNNLHKIKIFETGYSPEFENIGQIALKCGGLPLAI 335
Qy      354 VYVAGLL-KSKRTIEDKTYAKDVKSVTNDPDERCSRVGLSYDHLTSDLTCTLHFGI 412
Db      354 VYVAGLL-KSKRTIEDKTYAKDVKSVTNDPDERCSRVGLSYDHLTSDLTCTLHFGI 412
Qy      336 TVIAGLSKMGORLDKWKQIENAVSSVSTDEACQCMRYLALSYHHLPSHLKPCFLYFAI 395
Db      336 TVIAGLSKMGORLDKWKQIENAVSSVSTDEACQCMRYLALSYHHLPSHLKPCFLYFAI 395
Qy      413 FPEDSDIPVKNLMRSMWAEGLKLE--NDLGEVEKCOELVDRCGLVYVSKSRDGTIKR 470
Db      413 FPEDSDIPVKNLMRSMWAEGLKLE--NDLGEVEKCOELVDRCGLVYVSKSRDGTIKR 470
Qy      396 FAEDEIYVKNLVDMANAEGLNEEGKSIEEVPPTCINELVDRSLISHNLSFG-KIE 454
Db      396 FAEDEIYVKNLVDMANAEGLNEEGKSIEEVPPTCINELVDRSLISHNLSFG-KIE 454
Qy      471 SKCVHDLIYDLVREVENFIMNDIVLVSYPEC--SYLCMKQPFKRTGDEINCYCYG 527
Db      471 SKCVHDLIYDLVREVENFIMNDIVLVSYPEC--SYLCMKQPFKRTGDEINCYCYG 527
Qy      455 RCEMHDVTRRELREAR--NNMFVAVINGNSDQNSCAQSMOCSEKRSRISIHNDIELW 512
Db      455 RCEMHDVTRRELREAR--NNMFVAVINGNSDQNSCAQSMOCSEKRSRISIHNDIELW 512
Qy      528 CPYGLYRALLTPVNNQOLDHONNNLKTHTSYFSPHLEPLYVYVLSKVYHFKLLVLELR 587
Db      528 CPYGLYRALLTPVNNQOLDHONNNLKTHTSYFSPHLEPLYVYVLSKVYHFKLLVLELR 587
Qy      513 C-----RNS---EASHTITF---CGKFTVLELSRFLVAVLDLG 545
Db      513 C-----RNS---EASHTITF---CGKFTVLELSRFLVAVLDLG 545
Qy      588 HROIDGPREILSLIWLRLSL-----FSYGNFDPPEICRLNNLOTFTYQRRSDI 630
Db      588 HROIDGPREILSLIWLRLSL-----FSYGNFDPPEICRLNNLOTFTYQRRSDI 630
Qy      546 STCIPFPGSVGLSLHLKRLSCFNPCLOKQYRGSLANPSSIIIDPLSISLCLYQTKL 605
Db      546 STCIPFPGSVGLSLHLKRLSCFNPCLOKQYRGSLANPSSIIIDPLSISLCLYQTKL 605
Qy      631 -TVQRFNSDT--TFAETIWMOLRHLKLPREYLPDPSGVKGRHLDPSNLTQITISYL 687
Db      631 -TVQRFNSDT--TFAETIWMOLRHLKLPREYLPDPSGVKGRHLDPSNLTQITISYL 687
Qy      606 CFPPEYRDVYFPILPSEILTMPLRLKLCMGMYL--RSHPEIENR-LVLSIQCLHQ 661
Db      606 CFPPEYRDVYFPILPSEILTMPLRLKLCMGMYL--RSHPEIENR-LVLSIQCLHQ 661
Qy      688 SPCCTKEVINGIQNVKLGISGNDKDYKSPRDGGLPRNLLVYLOOELTSL----- 738
Db      688 SPCCTKEVINGIQNVKLGISGNDKDYKSPRDGGLPRNLLVYLOOELTSL----- 738
Qy      662 NPMYCTGTSFFRLIPNLKLVKGIQODFRNRKD--PYDFRYLQLEKLEFSIRPAGOV 718
Db      662 NPMYCTGTSFFRLIPNLKLVKGIQODFRNRKD--PYDFRYLQLEKLEFSIRPAGOV 718

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QY 739 -----ISVDYSL-----PVIISSAKFPAITLKKLE-RT 768
DB 719 AACILKNTAPSGSTPEQELRFOTELFHRTYFEMWETAPLTLPPDPAFONLKLSTFGRGEF 778
QY 769 YLSWYSLIITIAELPYLEVYLKMDACCGEEMPIYMGFRKLLKLLIKSFLKFWKATNDN 828
DB 779 FLAWMDLSIVGKLPKLEVLKLSYNPFKEWEVAEGEPHKLFLDLKVIYIKWRASSDH 838
QY 829 PVLRLIRISCKNLKEIPFIEADITHLQILIELRCPPKLGSAARIOKEODLGNPNVD 888
DB 839 PVLRLIRISCKNLKEIPFIEADITHLQILIELRCPPKLGSAARIOKEODLGNPNVD 898
QY 889 VRISNPL-----KESDSE 903
DB 899 VTRNLIVDSVTDEDDDD 920

RESULT 3
Q9SM52 PRELIMINARY; PRT; 938 AA.
ID AC Q9SM52;
DI 01-MAY-2000 (TREMBLrel. 13, Created)
DI 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DI 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE NBS-LRR PROTEIN.
GN RX2.ACI5.
OS Solanum acule (Wild potato).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCB1_Taxid=103871;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LEAF;
RX MEDLINE=20117531; PubMed=10652152;
RA Bendahmane A., Querol M., Kanyuka K., Baulcombe D.C.;
RT "Agrobacterium transient expression system as a tool for the isolation
RT of disease resistance genes: application to the Rx2 locus in potato.";
RL Plant J. 21:73-81(2000).
DR EMBL: AJ249448; CAB56299.1; ".
DR InterPro: IPR000767; Disease_resist.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR002182; NB-ARC.
DR Pfam: PF00560; LRR; 1.
DR Pfam: PF00931; NB-ARC; 1.
DR PRINTS: PR00364; DISEASERISIT.
SQ SEQUENCE 938 AA; 107529 MW; 43853213B07327AB CRC64;

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Query Match 26.4%; Score 1245; DB 10; Length 938;  
 Best Local Similarity 35.2%; Pred. No. 3.1e-75;  
 Matches 351; Conservative 139; Mismatches 330; Indels 176; Gaps 32;

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QY 1 MAHAYASLARTTESLTFNSPMQSLCDHREELCALREKVSLEYEVKNEKN-NWFG- 58
DB 1 MAYAAYTSIMKRTI-----HSMELHGC-----LQPPYELESTRAL---EKSANTGD 47
QY 59 -EMTDEVEVEVSAEAETIQLRTGLVGENKSOKKARRRPROSLQOAVADMHIW 116
DB 48 HEELITILEVLEAVATTEDMVDESRSVFLAONLEERNRAMEIFEVLEQALECIDSTV 107
QY 117 KESTKIODKKOVSKE--SLV-----HDESSSTDILKVKNNMGGRDOOROLLEDLRSY 170
DB 108 KQMMATSDSKKDLKPGTSSLSVSLPDHAF-----OPENIMVGREVEFEMLDQVYRG- 159
QY 171 SGEPKVIPIYMGIGIKTTIAKEEYNDSEILCREVDHAMATISQAHNKKELILGLHSTI 230
DB 160 GRELEVSIYMGIGIKTTIATKLYSDPIYMSRPDIRAKATVSGEYCVRVNVLGLSLSTS 219
QY 231 KMDRYAMICEAEIADMLOKSLKRRKRLIYLDIWSCEVNDGVAKRCPTEEDMAGSRILLT 290
DB 220 DEBD-----DQADRLQKHLKGRRLVYIDITWKAMDGIKLP--DQYKGSRIILT 271

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QY 291 TRNDEVACYAGVENSLSRMSFMDOESMELFKSAAPFSE-ALPYEFETVGOIADACHL 349
DB 272 TRNVEAEAEASSGKPPHNRKLMMFDESNNLKKLTKFEKGSYSPEPENIGKOLAKCGSL 331
QY 350 PLTIYVAGIL-KSKRTIEDMKTVAKDVSFYTNPDERCORYLGISYDLHLSDKLTCL 408
DB 332 PLATYIAGLLKISKITDEMQNVAENVSYSYSTDLEACRMVRLALSYHHLPSHLKPCFL 391
QY 409 HGEIPEDSDIPVKNIMRSMAAGFLKLE--NDLGEVEKCLQELVDRLVLSKRSRG 466
DB 392 YFAIFEDERISVTKLYELMAVEGFINEEGRKSIEEVAETCINELVDRSLISHNLSFG 451
QY 467 TKIRSKVNDLIYDLCVREORENIFIMNDIYADVSPGOSYLCMKMPKFKVTGDEIN 526
DB 452 -KIESCGMDVIRELCREAR--NMNFVNT-----RGKSDQ-N 486
QY 527 YCPYGLRALTFPVNRQLRDHDNNNLKRTHSVFSEHLEPLYYVLKSEV----- 575
DB 487 SCAGSMQSRFSK--RSRIH-----KLEELAMCRNSEAHSIIMLGFEFC 529
QY 576 ---VHFKILVLELRHROIDGFPREILSLMRLYSL-----FSYGNPD 616
DB 530 VLELSFKLVAVLDGLNTWPIPSGVLSLHLRYLSLRPNCLQOYQGSKEAVPSIID 589
QY 617 VPEELGRIMNLQTFEIVQ-RRSDI-IIFAEIEMQLRLKLPFRYLPDPCPGSYDKGR 674
DB 590 IPIISISLCYLOTFKLNLPSPSYPIPLSEIITFMQOLRLCDMWYL---RSHEPTENR 646
QY 675 HDFSNIQITISYSPRCCTKEVIMGIQNVAKLIGISGNKDDYKFSRSGLPNNIYVLOLE 734
DB 647 -LVKMLQCLNQNLNPRCTGSFFRLPNLKLQVFGVEPDEFRSSODL---YDRRYLYOLE 702
QY 735 ILSL-----ISVDYSL-----PVIISSAK 754
DB 703 ELTFRLYYPAACFLKNTAPSGSTPODPLRFOTELHKEIDFGTAPPTLLP-----PPD 758
QY 755 APPATLKKLTKERTY-LSMSYLDIIAELPNIYELKMDACCGEEMPIYMGFRKLL 813
DB 759 AFQONLKLSTFRREFSVAMKDLISVGLPKLEVLISLWNAFISGMVEVEGEPHNLFLF 818
QY 814 IKYSLFKWKATNDNPFVLELRIRISCKNLKEIPFIEADITHLQILIELRCPPKLGSA 873
DB 819 LDDVIYIRYWRASSDHFEYLERLILRDCRNLDSPRPADITTLALIDIDYQGSVNSAK 878
QY 874 RIKOEODLGNPNVDVRI-----SNPLKESDSDS 902
DB 879 QIQODIODNYGSSIEVTRHLFTPKSVTYVEDDDDS 914

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RESULT 4  
 ID AC Q9ST04 PRELIMINARY; PRT; 912 AA.  
 AC Q9ST04;  
 DI 01-MAY-2000 (TREMBLrel. 13, Created)  
 DI 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DI 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE NBS-LRR PROTEIN.  
 GN GPA2.  
 OS Solanum tuberosum (Potato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.  
 OX NCB1\_Taxid=4113;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=ROOT;  
 RA Bendahmane A., Kanyuka K., Baulcombe D.C.;  
 RT "Agrobacterium transient expression system as a tool for disease  
 RT resistance genes isolation: application to Rx2 locus in potato.";  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 SQ SEQUENCE FROM N.A.

RA Van der Vossen E.A.G.;  
 RL Submitted (OCr-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ249449; CAB55838.1; -  
 DR EMBL: AF195939; AF04603.1; -  
 DR InterPro: IPR000767; Disease\_resist.  
 DR InterPro: IPR001611; LRR.  
 DR InterPro: IPR002182; NB-ARC.  
 DR Pfam: PF00560; LRR; 2.  
 DR Pfam: PF00931; NB-ARC; 1.  
 DR PRINTS: PR00364; DISEASERST.  
 SQ SEQUENCE 912 AA; 104551 MW; 65EFD9C86686F76B CRC64;

Query Match 26.4%; Score 1242.5; DB 10; Length 912;  
 Best Local Similarity 35.1%; Pred. No. 4.4e-75;  
 Matches 340; Conservative 146; Mismatches 333; Indels 149; Gaps 29;

QY 1 MAHASIASIMRTIESLITFNSPMQSLSCDHRELCALREKVSLEVFYKNEKN-NVGE 59  
 DB 1 MAYAAVTSIMRTI-----HQMELTGCD---LQPFYEKLKSLAIL---EKSCNIMGD 47  
 QY 60 ---MTDFEVEVESAAYETIQLRTGLTVLGENKSQKKARRRROSIOQVAEDMDHIT 116  
 DB 48 HEGITLLEVEITTEVATTTEDVDSESRVFLARNKGRSRAMWGIFVLEALECIDSTV 107  
 QY 117 KESTRIODKGOVSKS--SLVHDFSSSTNDILKVNKNWGRDQKOLLEDTLSYSGEP 174  
 DB 108 KQWMTSDSMKDLKQTSLSV---SLPEHDVQPEINIMVGNREPFEMDOLAR-GREL 163  
 QY 175 KVIPIVGMGIGKTTLAKVYNDSEILCFDYHAWATISQOHKKKEILLGLHSTIKMD 234  
 DB 164 EVASIVGMGIGKTTLAKVYNDSEILCFDYHAWATISQOHKKKEILLGLHSTIKMD 223  
 QY 235 RVKMGELADMLCKSLKRRYLVLDIDVSCVWDVGRCFEPEDNAGSRILITTRND 294  
 DB 224 ---YQLADQLOKHLKGRYLVVDDIWTTEAMDILKCFPCDDN-GSRILITTRNV 275  
 QY 295 EVACYAGVENFSLRMSFMDODESMFLKSAFSS-ALPYEFYVGOQIADCHGLPLTI 353  
 DB 276 EVAEYASGKPRPHMRLMNFDESNNLHKKIFKEGSSPEFENIGQIALKCGGLPLAI 335  
 QY 354 VYVAGLL-KSKRTIEDKTVAKDVSPVTNDDEKSRVLGISTHLSLSDKTLIHGCI 412  
 DB 336 TLIALCLIKISTYDEWONAVENRVSSTDEAKCMRYLALSYHRLPSHLKPCFLYPAI 395  
 QY 413 FPEDSIDIVKNIIMRSMAGELKLE--NDLEGEVEKLOELVDRGLTVYKSRSDGTKR 470  
 DB 396 FAEDRIYVNNKLVELMAVEGLNEBEGKSIEVAETCINELVDRGLISIHVSPDG-ETQ 454  
 QY 471 SKVADLIYDLCEVQRENTIFIMNDIYLDVSYPC--SYLCMYKQPEKRYTGDEINVC 528  
 DB 455 RCGMDVTRICLREAR--NNMFVAVIRGKSDQNSCAQSMCCSFKR----- 499  
 QY 529 PYGLRALLFTFVNRQLRHDNNNL---KTHSVFSLHLEPLIYVVKSEVYHFKLVL 584  
 DB 500 -----SKTSHNEBELWCNSENSEHSTITLCI---FKCVTLSEFLVLRV 542  
 QY 585 ELRRHRODGFPELILSLIMRLYSL-----FSYGNFVDPPEICRLMNTOT 629  
 DB 543 DLGLTCTGFPSGVLSLHLRYLSRFPRLQYRGSKENAPSSIDIDPLISISLCYTQT 602  
 QY 630 F-IYQRRSDI-TTFAETIWMOLRIKLDRFYLPDCPSGVKGRHLDFSNLOTISYL 687  
 DB 603 FKLHHPNCYRFLPSILTMPQLRKLCGMWNL---RSHEPTENR-LVLSLQCLNEL 658  
 QY 688 SPRCCTKEVINGIONVKKLIGISGNKDYKSPRDSGLPNNLVLVYLOOLETSLISVDYS--- 744  
 DB 659 NPKCTGSLFLFNLKLEVFYKEDRNKDL---YDFRILVQLELA-FSTYYSSEA 714  
 QY 745 -----LLPVIISAKAPATLKK 762  
 DB 715 CELKNTAPLGSTPDPLRFQWETLHLETHSRATAPPTDVTFFLLP-----PPDCFPQNLKS 770

QY 763 LKLERT-YLSWSTYLDIAELPNEVLKLMDDACCGERMHPYVGFNRLKILIKISFLK 821  
 DB 771 LTRSGDFELAMKDLSTVIGKLPKLEVLQLSHNAKGEWEVEGFPKLPFLDSITYRY 830  
 QY 822 WKATDNFVYLERIMTRSCNKLKEPIEFADITHLQILRECPKLGESANRIKOEQD 881  
 DB 831 WRASSDHFPYLERLFLSDCYLSDIRDFADITTLALIDIFRCQOSGNSAKQIQQDID 890  
 QY 882 LGNNPYDV 889  
 DB 891 NVGSIEV 898

RESULT 5  
 ID Q9XGF5 PRELIMINARY; PRT: 937 AA.  
 AC Q9XGF5;  
 DT 01-NOV-1999 (TREMBLrel, 12, Created)  
 DT 01-NOV-1999 (TREMBLrel, 12, Last sequence update)  
 DE 01-JUN-2001 (TREMBLrel, 17, Last annotation update)  
 DE RX PROTEIN.  
 GN Solanum tuberosum (Potato).  
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; eunasterids I; Solanales; Solanaceae; Solanum.  
 OX NCBI\_TaxID=4113;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. CARA;  
 RX MEDLINE=99264301; PubMed=10330465;  
 RA Bendahmane A., Kanyuka K., Baulcombe D.C.;  
 RT "The Rx gene from potato controls separate virus resistance and cell  
 death responses.";  
 RL Plant Cell 11:781-791(1999).  
 DR EMBL: AJ011801; CAB50786.1; -  
 DR InterPro: IPR000767; Disease\_resist.  
 DR InterPro: IPR002182; NB-ARC.  
 DR Pfam: PF00931; NB-ARC; 1.  
 DR PRINTS: PR00364; DISEASERST.  
 SQ SEQUENCE 937 AA; 107489 MW; 98F96B2BE31D3490 CRC64;

Query Match 26.2%; Score 1234.5; DB 10; Length 937;  
 Best Local Similarity 35.1%; Pred. No. 1.6e-74;  
 Matches 345; Conservative 144; Mismatches 343; Indels 131; Gaps 32;

QY 1 MAHASIASIMRTIESLITFNSPMQSLSCDHRELCALREKVSLEVFYKNEKN-NVGE 59  
 DB 1 MAYAAVTSIMRTI-----HQMELTGCD---LQPFYEKLKSLAIL---EKSCNIMGD 47  
 QY 60 ---MTDFEVEVESAAYETIQLRTGLTVLGENKSQKKARRRROSIOQVAEDMDHIT 116  
 DB 48 HEGITLLEVEITTEVATTTEDVDSESRVFLARNKGRSRAMWGIFVLEALECIDSTV 107  
 QY 117 KESTRIODKGOVSKS--SLVHDFSSSTNDILKVNKNWGRDQKOLLEDTLSYSGEP 174  
 DB 108 KQWMTSDSMKDLKQTSLSV---SLPEHDVQPEINIMVGNREPFEMDOLAR-GREL 163  
 QY 175 KVIPIVGMGIGKTTLAKVYNDSEILCFDYHAWATISQOHKKKEILLGLHSTIKMD 234  
 DB 164 EVASIVGMGIGKTTLAKVYNDSEILCFDYHAWATISQOHKKKEILLGLHSTIKMD 223  
 QY 235 RVKMGELADMLCKSLKRRYLVLDIDVSCVWDVGRCFEPEDNAGSRILITTRND 294  
 DB 224 ---DQLADRLQKHLKGRYLVVDDIWTTEAMDILKCFPCDN-GSRILITTRNV 275  
 QY 295 EVACYAGVENFSLRMSFMDODESMFLKSAFSS-ALPYEFYVGOQIADCHGLPLTI 353  
 DB 276 EVAEYASGKPRPHMRLMNFDESNNLHKKIFKEGSSPEFENIGQIALKCGGLPLAI 335  
 QY 354 VYVAGLL-KSKRTIEDKTVAKDVSPVTNDDEKSRVLGISTHLSLSDKTLIHGCI 412



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Db 336 TVIAGILSKMGRLDEMORIGENSVSTDEPAOCMRVLAISTHHLKPCFLYFPI 395
Qy 413 FPEPDSIDIPKNIIMRSMMAEGFLKLE--NDLEGEVEKCELOELVDRCLVYKSRSDGTR 470
Db 396 FREDQOISNELVELMPVGFLENEEGKSIEEVAUTCINELDRSLIFHNPSFRT-1E 454
Qy 471 SCKVHDLIYDLCEVREVORENIFIMDIYLDVSYPECCSYLCMKMOPFKVYDGEINCY 530
Db 455 SCGMHVDVRELCREAR--NMNFVNYI-----RGKSDQ--NSCAQ 490
Qy 531 GLYRALITPVNQLDHDNNLL-----KTHSVF--SPHEPLVYVLKSEVYHFKLV 583
Db 491 SMOGRSEKS--RSRIKHVEELAMCRNSEASHIMLGFEVYTL-----ELSEKLVAV 541
Qy 584 LELRHROIDGFPREILSLIMLYLSTL-----FSGNFDVPPETICRLMNO 628
Db 542 LDGLNTWPIFFSGVSLHLHRYLSRFNPCLQOYGSKAVPSSIIDIPLSISLCYIO 601
Qy 629 TTVVO-REFSDI-IIFAEIWEMLQRLKLPFYLPDPPSGSVCKGRHLDPENQITISY 686
Db 602 TKLNLPEFSYYPFLIPSELTPMLPRLCMGNVYL--RSHEPTENR-LVKNLQCLMO 657
Qy 687 LSPRCTKRVINGIOWKKGISGNKDYKSPFDSGLPNNLVYLOLELSTL-----738
Db 658 LNPRTYGTSGFPLRFLKTKLOVGVPEDEFRNSQDL--YDFRYLYQLEELFRLYYPAA 714
Qy 739 -----ISVDYS-----LPLVITSSAKAPATIKLKLK 767
Db 715 CELKNTAPSGSTODPLRFOTELIHKEDFGTAPPLLP---PPDAPPOINKSLTFRC 770
Qy 768 TV-LISVYDITIAELPNLEVLKIMDACCGEWHPIVMGFNRLKLLIKYSPFKWATN 826
Db 771 ERSVAKDLSIVKLEKLEVLISNNAPFKSEVYVEEGPHLKLFLDLYVIRYMRASS 830
Qy 827 DNEPVLERTMIRSKNLKEIPFADITHTLQLELRECPKIGESAAIROKECEDIGNP 886
Db 831 DHPYLERVILRDCRNLDSPROFADITLALIDYCCQSVNSAKOIODIDYNGSS 890
Qy 887 VDVRI-----SNPKESDSDS 902
Db 891 IEVTRHLFLPKSVTVEDDDDS 913

RESULT 6
Q9LID4 PRELIMINARY; PRT; 1824 AA.
AC Q9LID4;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE PRF.
OS Lycopersicon pimpinellifolium (Culant tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; easterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4084;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. RIO GRANDE 76R; TRANSPOSON-RETROTANSPOSON TOTOT;
RA Lavelle D.T., Oldroyd G.E.D., Dalbeck D., Staskiewicz B.J.,
RA Michelmore R.W.;
RT "the structure and evolution of the Pto locus in tomato.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF20602; AAF76308.1; -
DR InterPro: IPR000767; Disease_resist.
DR InterPro: IPR001916; Lactalbumin_lysozyme.
DR InterPro: IPR002182; NB-ARC.
DR Pfam: PF00931; NB-ARC; 1.
DR PRINTS: PR00364; DISEASERISF.
DR PROSITE: PS00128; LACTALBUMIN_LYSOZYME; UNKNOWN_1.
SQ SEQUENCE 1824 AA; 209574 MW; 1F14E7D662DEBAC6 CRC64;

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Query Match 20.8%; Score 980; DB 10; Length 1824;
Best Local Similarity 30.9%; Pred. No. 56-57;
Matches 288; Conservative 167; Mismatches 342; Indels 136; Gaps 33;

Qy 26 LSCDREELCALREKVSLEVEYKNE-EKNVFGEMTDEVEVEYASAEYI-----78
Db 972 LIIDLKHOLESYKESGLCRSFIDHSESDEHDEACGLIARVSVAAYAEVYIDSCLAY 1031
Qy 79 -----QRLTGVLDENKSQKKARRRPROSLQOYAEEDHDMKSTKL 122
Db 1032 SHPLWYKVLWISEVLEENIKVYKNVGETCE-----RRNIEVYHEVAKTTTY-----1079
Qy 123 QDKGRVSKESLVHDESSGNDLTKVKNMVGGDDROKOLEDTFTSSYSGEPK--VIPTV 180
Db 1080 -----APFSATQ-----RANEMEGQDITDELKDL-----LGGSPELVYSIV 1121
Qy 181 GMSGIGKTTLAKEVYNDESILCFDYHAMATYSQHNKKEITLGLHSTIKMDPRKMIG 240
Db 1122 GMPGLKTTLAKKIYNDPEVTSRFDVHAOCVYQLYSMRELTLTILNDVLEPSDRNEK-E 1180
Qy 241 EELADMLQKSLKRRKRYLYVLDIOWSCVWDVGRCEPTEDNAGSRILTTNRDEVACYA 300
Db 1181 DGEIADBLRFLTKRFLIIDDVMDKYVNDLCEGSDVSNR-SRIITLTRLNDVAEYV 1239
Qy 301 GVENFSLRMSFMDQDSWSLFSKSAFSSALPYEFETVGQIADDECHGLPLTYVYAGLV 360
Db 1240 KCESDPHHLRLFRDDESWTLQKEVEFGESCPPELEDVGEISKSGCLPLSVYLVAGVL 1299
Qy 361 K-SKRTIEPMKYAKOVKSVTNDPDERGSRVGLSYDHTLSDTKTLHFHGFPEPDSI 419
Db 1300 KOKKKTLDMSKVVQEOSLSORISLESIS-IIGFSKNIPLHYKPGFLIFGGILOGKDI 1358
Qy 420 PKNLMRSMMAEGFLKLEND--LEGEVEKCELOELVDRCLVYKSRSDGTRKIRSKYVHL 477
Db 1359 HYSKMTKRLWABEGVQVANNKGEQDFAQGLDLDIGANNVAMAK-RPNKTKVKTCRIHDL 1417
Qy 478 IYDLCVREVORENIFIMDIYLDVS-----YPECSTYLCMKMOPFKVYDGEINCYCYGL 532
Db 1418 LHKFMEKAKQE-----DELLQINSGEGVPE--RLEERYL--FVHYSODEID-----L 1462
Qy 533 YRALITPVNQLRDH--DNNNILKTHSVFSPHEPLVYVLKSEVYHFKLVLELRHQI 591
Db 1463 WRPSRSNVRSILFENADIDPNLMPRDISFTPE-----SKLYVYLDLESFNI 1509
Qy 592 DG-FPREILSLIMLYLSTLSYGNFDVPPETICRLMNLQTFIVQFRSDIIFAEIWEML 650
Db 1510 GGFPTPELOYLQMKYFAAQTDAN-SIPSSIAKLENIETFEVVRGIGEMILPC-SLTKMV 1567
Qy 651 QLRHLKLPRLYLPDPPSGSVCKGRHLDP-----NLOTISYLSPRCC-----TKEVI 697
Db 1568 KLRIHIV-----NDRVSGFHEHNDVLTGNSOLPNETFS--PRFLYFGDAEKVL 1616
Qy 698 MGIONVKKL-----GISGNKDYKSPFDSGLPNNLVYLOLELSTLSVDYSLPVISS 752
Db 1617 KMKPKLKLKLSIGTGTGYSKLLG-KCYRRP-RLDPLSHLESIAKIVNSV---PAKLP 1671
Qy 753 AKAPATLKLKLETRYLSWSYDIIAELPNLEVLKIMDACCGEWHPIVMGFNRLKLL 812
Db 1672 KFNPPSOURELTLSKFLRPLWQISIIAELPNLVILKILLRAFEGHWEVKNSEFLEKYL 1731
Qy 813 LKISFLKFKWATNDPNPVLRLMIRSKNLKEIPFADITHTLQLELRCPKIGESA 872
Db 1732 KLIDMLKVQWQSIDAPAFKLELHVLTKKHLKIPSRDEAVCLARVEVNMNANSA 1791
Qy 873 ARIQKEO-EDLGNPVDYRISNP--LKESDSDS 902
Db 1792 ODITQMOHEVIANDSFYVTIOPPMKSKQPIIDS 1824

RESULT 7
Q96485
ID Q96485 PRELIMINARY; PRT; 1824 AA.
AC Q96485;

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DT 01-FEB-1997 (TREMBlrel. 02, Created)  
 DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE PRE.  
 GN Lycopersicon esculentum (Tomato).  
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 CC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.  
 CX NCBI\_TaxID=4081;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RIO GRANDE;  
 RX MEDLINE=96291405; PubMed=8689679;  
 RA Salmemon J.M., Oldroyd G.E., Rommens C.M., Scofield S.R., Kim H.S.,  
 RA Lavelle D.T., Dahlbeck D., Staskawicz B.J.,  
 RT "Tomato Prf is a member of the leucine-rich repeat class of plant  
 RT disease resistance genes and lies embedded within the Pto kinase gene  
 RT cluster."  
 RL Cell 86:123-133(1996).  
 DR EMBL: U65391; AAC49408.1;  
 DR InterPro: IPR001916; Lactalbumin\_Lysozyme.  
 DR InterPro: IPR002182; NB-ARC.  
 DR Pfam: Pf00931; NB-ARC; 1.  
 DR PROSITE: PS00128; LACTALBUMIN\_LYSOZYME; UNKNOWN.1.  
 SQ SEQUENCE 1824 AA; 209588 MW; B6A63CEACA98EB2 CRC64;

Query Match 20.8%; Score 980; DB 10; Length 1824;  
 Best Local Similarity 30.9%; Pred. No. 5e-57;  
 Matches 288; Conservative 167; Mismatches 342; Indels 136; Gaps 33;  
 QY 26 LSCDHREELCALREKVSLEFVKNF-EKNNVFGEMLDFEVEYEVASAEYTI----- 78  
 DB 972 LIIDLKHOIESVKEGLCLCRFIDHFSYDEHDEACGLIARVSMAYKAELYDISCLAY 1031  
 QY 79 -----QLRLGTVLGKNSQKKARRRFRSLOQVADMDHIMKESTKI 122  
 DB 1032 SHPLMYKVLMISEVLNIKLVKNVGETCE-----RRNIEVTVHEVAKTYTYV----- 1079  
 QY 123 QDCKQOVSKESLVHDESSSTNDILKVKNNMVGRRDQRRKOLLEDLTRSYSGEPK--VIPIV 180  
 DB 1080 -----APSFSAVYTO--RANEEMEGFODTIDELDKDL--LGSPBELDIYSIV 1121  
 QY 181 GMSGIGKTTLAKEVYNDESILCRFDVHAMATISQHNKKEILLGLHSTIGMDEVRKMG 240  
 DB 1122 GMPGLGKTTLAKKIYNPEVTSRFDVAHACVVTQLYSWRELLITLNDVLEPSDRNEK-E 1180  
 QY 241 EAEIADMLQSLAKRRKYLIVDDIWSCEVMDGVRCRPTEDNAGSRILLITRNDVACYA 300  
 DB 1181 DGEIADMLRRLTLKRLPLILDDVDWYKVMWNLQCMCFSDVSNR--SRILLITRLNDVAEYV 1239  
 QY 301 GVENFSLRMSFMDQDESMSLFKSAFSSALPYEFETVNGKIOADECGILPLTIYVAVGL 360  
 DB 1240 KCESDPRHLRLFRNDESWTLLOKREVFQGESCPRELEDDVGFPISSCGPLSVLVAVGL 1299  
 QY 361 K-SKRTIEDMKYAKDVCSFYTNDPDERGSRVGLSYDHLTSDIKTGLHFGIRPEDSDI 419  
 DB 1300 KOKKKTIDSKVYVQOSLSRIGSLSEISIS-ILGFSYKNIPLHYLKPGLVFGGLQCKDI 1358  
 QY 420 PVKILMSMAEGLKLEND--LEGEVEKLOELVDRCLIVLSKRSRDKIRISCKVHDL 477  
 DB 1359 HVSAMTKLMAEGLVQANNKGGEDTAQGLDILIGRNVAMERK-RPNKRVKTCRIHDL 1417  
 QY 478 IYDLQVREVORENIFINNDIVLQVS-----YPECSYLCKMKMOPFKRVTGDEIYCPYGL 532  
 DB 1418 LHKFCWEKAKOE-----DFLQINSGEVPE--RLEEVRL--FVHSYODEID-----L 1462  
 QY 533 YKALLTIVYNQLRDH--DNNULKRTKHSVFSFHLPELYLVKSEVHFKLLKVLRLRQI 591  
 DB 1463 WRSSRSNVRSLFNALDPDMLMPRDISIFTE-----SRKLVKVLDDLESFNI 1509  
 QY 592 DG-FPREILSLIMRLYLSFSYGNFDPPEICRLMNQFTIYVGRFRSDIILFMEIWEIM 650

DB 1510 GCTFPREIYLIQMKTFPAQOTAN-SIPSSIAKLENLEFFVGRGEGMILPC-SILKAV 1567  
 QY 651 QLRHLKLPFRYLPDPCSGSVDRGRHLDFS-----MAQTIYSPPGCC-----TKREVI 697  
 DB 1568 KLRHIIHV-----NDRVSFGLHENMDVLGNISQLPLERFSS--TPRLFGKDAEKVL 1616  
 QY 698 MGIQWVKL-----GISGKKDYKSRFSDGLRNRLVYLOQLEILSLISVYSLLPYIIS 752  
 DB 1617 RMPKRLKRLSCIFSGTFGYSRLKLG-RCVRP-RIDFLSHLESLKIVSNSY--PAKLPH 1671  
 QY 753 AKAPATLKLKLEERTYLSMSYLDIIAELPNLEVLKIMDACCGEEMHPIVGFNRKL 812  
 DB 1672 KNFESQRLBELTSLKFRPLWTOISIAELPVLIIKLRLAEGHWEKDSFELKYL 1731  
 QY 813 LKYSFLKFWKATDNFVYLERIMTRCKNLKEIPFEADIIYLIQLELRECPKIGESA 872  
 DB 1732 KLDNLKVVQWSISDDAFKLEHLVLTCKKLEKIPSRFEDAVCLARVEVMCMNVYANSA 1791  
 QY 873 ARIQEQ-EDLGNNVVDRIISP--LKESDSDS 902  
 DB 1792 QDIQTMHEVIANDSFTYTIQPPDWSKQPLDS 1824

## RESULT 8

ID Q9ILD0 PRELIMINARY; PRT; 1825 AA.  
 AC Q9ILD0;

DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE PRE.

OS Lycopersicon esculentum (Tomato)

CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

CC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

CX NCBI\_TaxID=4081;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. VINT CHERRY; TRANSPOSON-RETROTRANSPOSON TOP1EL;

RA Lavelle D.T., Oldroyd G.E.D., Dahlbeck D., Staskawicz B.J.,

RA "The structure and evolution of the Pto locus in tomato."

RT Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.

DR EMBL: AF220603; AAF76312.1;

DR InterPro: IPR0006767; Disease\_resist.

DR InterPro: IPR001916; Lactalbumin\_Lysozyme.

DR InterPro: IPR002182; NB-ARC.

DR Pfam: Pf00931; NB-ARC; 1.

DR PRINTS: PR00364; DISEASERESIST.

DR PROSITE: PS00128; LACTALBUMIN\_LYSOZYME; UNKNOWN.1.

SQ SEQUENCE 1825 AA; 209596 MW; 413913A1C067E24D CRC64;

Query Match 20.6%; Score 970; DB 10; Length 1825;  
 Best Local Similarity 31.0%; Pred. No. 2.3e-56;  
 Matches 288; Conservative 168; Mismatches 345; Indels 128; Gaps 34;



Db 1133 EYLOL-HDVCFPOSEECLODITFHKKLLKLYKLNISR-WDYSESFLLETLVTKCI 1190

QY 842 NLKEPIEFADITLQIIEI-RECPKLGESARIOKEOD 881

Db 1191 DLKEPIEFADITLQIIEI-KLIGSKWVSLSDSAVAKKEIKD 1231

RESULT 10

094109 PRELIMINARY; PRT; 1245 AA.

AC 094109

DT 01-DEC-2001 (TREMblrel. 19, Created)

DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)

DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)

DE TOSPOVIRUS RESISTANCE PROTEIN A.

GN SW5-A.

OS Lycopersicon esculentum (Tomato).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

OC NCBI\_TaxID=4081;

OX

RP SEQUENCE FROM N.A.

RC STRAIN-CV. STEVENS;

RA Folkertsma R.T., Spassova M.I., Prins M., Stevens M.R., Hille J.,

RA Goldbach R.W.;

RT "Construction of a bacterial artificial chromosome (BAC) library of

RT Lycopersicon esculentum cv. Stevens and its application to physically

RT map the Sw-5 locus."

RT Mol. Breed. 5:197-207 (1999).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-CV. STEVENS;

RA Prins T.W., Spassova M.I., Prins M., Klein Lankhorst R.,

RA Folkertsma R.T., Hille J., Goldbach R.W.;

RT "The Sw-5 locus confers resistance to Tospoviruses."

RT Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY007366; AAC31013.1; -

SO SEQUENCE 1245 AA; 143538 MW; 251BEFAS8FB00B46 CMC64;

Query Match 18.6%; Score 875.5; DB 10; Length 1245;

Best Local Similarity 29.2%; Pred. No. 3.1e-50;

Matches 272; Conservative 167; Mismatches 341; Indels 153; Gaps 33;

QY 8 SLMTIESILTFNPSMOSLSDHRELCALREKSSLEVVKNKFNKNGEMTD----- 62

Db 394 SLKRLKEMSTSKSGLGFLM--KPLGKLEKELSLTSLIEK-ELSSIFSVDVHHEHNT 449

QY 63 -----FEVEYEVASAEYTIQRL--TGTVLGENKSKQKKARRFRFOSIQ 107

Db 450 PKDQRTINLAIEVAIDSLAQYNAFLHIFCSLPTIYE-----IKQ 494

QY 108 VAEDMDIWEKSTKIQDKGVKSVLHDESSSTNDILKYNKNGRDQKQLEDLT 167

Db 495 INVEVTEKMSDIDPLNHYVAAPLKHLPDRHSNLYTD-----EEVVGFEKQAEELIDYL 549

QY 168 RSYGGEVPVPIVGMGGIGKTTAKVEYNDSESLCRFDVHAMATISQOHKKEILGLH 227

Db 550 RG-TNELDVVPVIGMGGGKTTAKKLINDIYSRFDVAMCITISQYKIELLDIDFS 608

QY 228 STIKMDRVMKIGAEALADMLQSLKRRRYLIVDDIMSGEVDGVRCPTEEDNAGSRI 287

Db 609 QVTGFNDGATVD--VLADMLRRLKMRKRYLIYDDMDMDMWDMLRLSP-DVGIRSI 665

QY 288 LITTRNDENVACYAGVENSLMSFMDQESWLFKSAFSEALPYFETVGAQIADCH 347

Db 666 VVTRLEEVGKQVYKHTDPSLPLTIEESQQLQKKVFOKECDPLTELQVSAVAEKCK 725

QY 348 GLPLTIYVVAALLSKRIEDMKTVARD-VKSFYTNPDRCRSVGLSDHLTSDKTC 406

Db 726 GLPLIYVVAIGAIKKRKKEESMNEVKALEPLDSEFESESLATMQLSPDNLPCHLKPC 785

QY 407 ILAHGIFPEDSDIPVKNLMSRMAGFLKLEND-----LEGEVEKLOELVRCGLVSK 461

Db 786 LLYMGAFESDARIIPASTLISMTIAGF--VENTESGRLEEBEABEYLMDLSSNLVMSK 843

QY 462 RSRDGKIRISCKVHDLIDYLCREVORENIFIMDVLDSVPECCSLCMYKMPFRKVT 521

Db 844 RSYKG-KYKYGQVHVHNFCL-EKSRKAFML-----AVK 877

QY 522 GDEINCPYGLYRALLTPVNRQLRDHNN--NLKRTSVSFHLEPL-----YV 570

Db 878 GOCIOFOPSD-WKG--TRVSFSELSKFSVSKTKPFRQHLITTTNRAKSIDVI 934

QY 571 LKSEVHVFLLKVLLETRHQIDGFPREILSLIWLTYLSFY-----GNFVPEICFLW 625

Db 935 LFCQISELRLLVLDL-----SYVEFLSLAKFPLQKLYLVAKKAFYFDG-SILP 988

QY 626 NLQTFIVORFRSDIIFAEELWMLQRLHLKPRYLPDCPSGSYDK-GRHLDSNLOT- 683

Db 989 HIETFIKRFYCGMGL-PVSEFMKKLRHAF-----GNAEFDKOGLFEGSSTLENL 1039

QY 684 -----ISYISPRCCTKEVIMGTONVYKKIGISGNKDDYKSFRRSGLPNNLVYLOQ 732

Db 1040 RLKNIIGFDGVLSRR-----PNIQQLDITFGNDEEFTPK--LENLTQLOQ 1088

QY 733 LEILSLISVDSLPLVLISSAKAPATLKLKLERTYLSWSYLDIABLPLVLEKLMD 792

Db 1089 LQL-----SFARPHLSGLQPSNLKLVLEGHIE-SVISIACLPSLEYQL-QD 1138

QY 793 ACC--GEEMHPVYMGFNRLKLLIKYSPLFKATNDNPFVLERMTSKNKEIPEEF 850

Db 1139 VCFPOSEECLODITFPKIKLKLVLNPLPSRWDVSESEFPLETFVVIKCDLEPIPSF 1198

QY 851 ADIHTLOIIEI-RECPKLGESARIOKEODL 882

Db 1199 VDIPIEQIKLIGSKWVSLSDSAVAKKEIKDI 1231

RESULT 11

094105 PRELIMINARY; PRT; 1241 AA.

AC 094105

DT 01-DEC-2001 (TREMblrel. 19, Created)

DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)

DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)

DE TOSPOVIRUS RESISTANCE PROTEIN E.

GN SW5-E.

OS Lycopersicon esculentum (Tomato).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

OC NCBI\_TaxID=4081;

OX

RP SEQUENCE FROM N.A.

RC STRAIN-CV. STEVENS;

RA Folkertsma R.T., Spassova M.I., Prins M., Stevens M.R., Hille J.,

RA Goldbach R.W.;

RT "Construction of a bacterial artificial chromosome (BAC) library of

RT Lycopersicon esculentum cv. Stevens and its application to physically

RT map the Sw-5 locus."

RT Mol. Breed. 5:197-207 (1999).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-CV. STEVENS;

RA Prins T.W., Spassova M.I., Prins M., Klein Lankhorst R.,

RA Folkertsma R.T., Hille J., Goldbach R.W.;

RT "The Sw-5 locus confers resistance to Tospoviruses."

RT Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY007367; AAC31017.1; -

SO SEQUENCE 1241 AA; 143224 MW; EF64DCDEC0378082 CRC64;

Query Match 18.3%; Score 864; DB 10; Length 1241;

Best Local Similarity 30.5%; Pred. No. 1.8e-49;

Matches 277; Conservative 163; Mismatches 327; Indels 142; Gaps 35;

```

QY 35 CALREVSSLEVFVKFEK-----NNVFGEMTDFEVEYREVASAETITQLRLTGTVLGE 89
DB 393 CMNEKQSTL---ISMLEKELSSLSIFPDVTKVHEHNDL---QRTTNLAYEAGVSD 446
QY 90 NKSOKKARRRPROSLOQVAEDMDHIMWKESTKIQDGKOVSKESLHDF-----SSST 142
DB 447 SICAKYNVWHCCSLPTLLEIKQINAEYTEMMSADILNPIYVAPKRLPTRRSNPI 506
QY 143 NDLKYNKNNVGRDQKOLLEDLRSYSGEPKVIDYVNGGIGTKTTLAKVYNDSEIIC 202
DB 507 TDEEYDEEIVGEGIDKEKTIQCLLNG-TNDLDYVPIVGGGCGKTTIARKVYNSDNIVS 565
QY 203 REDVHAMATISQOHNKEKILLGLHSTIKMDRVKMIGEAELADMOKSLKRRYIIVLD 262
DB 566 HEDVRAWCIYVQTYNRKLLQELTLOVTSKSD--KGEYDILADELRKSLKMGRIYIIVLD 623
QY 263 DIMSCVMDGVRCFPTEDNAGSRILLTTR---NDEVACYAGVENFSLRMSFMDQESW 318
DB 624 DMWDCAMMDLRLSPDFEGNR-SRIYVTRLEKVGQVCH--TDPYSL--PRLTTEBSC 678
QY 319 SLFKSAFSSSEALPYEFETVQKQIADCHGLPLTIVVAGLLKSKRTIEDMKTAVDVNS 378
DB 679 KLLQKVFQKEDCPPEIQOVSVAEKCKGLPLVIVVAGIIRKRMEBSMNELKDSILF 738
QY 379 FYTNPDDECSR-VLGLSTDHLSDTKLTLLHGIIFPESDIPYKMLMSMAEGKLKE 437
DB 739 DYLDCHSEGYSTRATMQLSDNLADLCKPLLYMGMPEDACIKVSLSLTMAEDVQ-- 796
QY 438 NDLEGEVEKLOELVRCILVNSKRSRDTKIRSCVHDLIYDQREYORENFIIFM--- 494
DB 797 -NIE-SAEYILANLISNVNMSKEYNG-KIKYCEVHNVYHLFCLEKSEENFMJLVANG 853
QY 495 -----NDIADVSYPECYILCMQKPFKRYTGEINCYPGYLRALLTPVNRQLDHND 549
DB 854 NNSQFSPWAKS--RVSPSLSENSKFAASKT---RKCSHQLRSLIT----- 896
QY 550 NMLKRTHSVFSEHLEPLYYVLAKEVYHFKLLKYLELRHQRQIDGFRREILS-LIMLRYS 608
DB 897 -----NGASFEDI---ISLSWIMHNLRLKVLVLSNHEWDTVNSATLKPRLNHLKYLG 944
QY 609 LFS---YGFNDVPEICRLMNLQTFVQRFSDIIFFAEIEWLMQRLHLKLPREFYLPDC 665
DB 945 VRAITFY--FD---RESHLPHLETILYKNDRS--VMLRCGFMEDLRIVEI----- 989
QY 666 PEGSYDK-GRHLDFSMLQTI-----SYLSPRCCTKEVIMGIQVYKGLGISG 710
DB 990 SDAEFQKGLFEGSSKLEMLRLIKNIYGFPIRADVLSRRC-----PNLQGHIEF 1040
QY 711 NKDDYKSPFSDSLPNNLVYLOQLLEISLISVDYSLPIVSISSKAPPAITLKIKLEERTYL 770
DB 1041 SIDEADSFCLTLEN---LTQLOKRLRISTECHSVL---SRLQJPSMIKKIKVLSNTCI 1091
QY 771 SMSYDILIELPNLEVLKILMD-----DACCGEEMHPIVNGFENIKLLIKYSLFKM 822
DB 1092 E-NLISFLEGLSLLEYLOLRDIYFPHQSKCKLGD-----ITFHKLILKLKLVQDISRW 1144
QY 823 KATNDNPFVLEIRLMIRSCNKLKIEPIEADITHTLOLIELRECPK-LGESAARIQEOED 881
DB 1145 DVSSEESFPLETIIIRRCNTEIEPISFADVPTLKQIKLILHCKKSLDSSAVRIKQDVED 1204
QY 882 -LGNRPVDY 889
DB 1205 NEGNDRIDL 1213

```

RESULT 12  
081136  
ID 081136 PRELIMINARY; PRT: 1255 AA.  
AC 081136;  
DT 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)

```

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PLANT RESISTANCE PROTEIN (DISEASE RESISTANCE GENE HOMOLOG MI-COPY1).
GN MI-1.1.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. VENT CHERRY; TISSUE=UNINDUCED ROOT;
RX MEDLINE=98374252; PubMed=9707547;
RA Ross J. M., Goggin F. L., Milligan S. B., Kaloshian I., Ullman D. E.,
RA "Williamson V.M.;
RT "The nematode resistance gene Mi of tomato confers resistance against
RT the potato aphid.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:9750-9754(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. VENT CHERRY; TISSUE=UNINDUCED ROOT;
RA Milligan S.B., Bodeau J., Yaghoobi J., Kaloshian I., Zabel P.,
RA Williamson V.M.;
RT "The root knot nematode resistance gene Mi from tomato is a member of
RT the leucine zipper, nucleotide binding, leucine-rich repeat family of
RT plant genes.";
RL Plant Cell 10:0-0(1998).
RN [3]
RP SEQUENCE OF 52-1255 FROM N.A.
RC STRAIN=CV. MOTELLE;
RA Bodeau J.P., Kaloshian I., Milligan S., Williamson V.M.;
RT "Isolation and large-scale sequencing of bacterial artificial
RT chromosomes (BACs) spanning the tomato Mi1 nematode-resistance
RT locus.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF039681; AAC67237.1; -.
DR EMBL; U81378; AAC32253.1; -.
DR InterPro: IPR001064; CrystalIn.
DR InterPro: IPR000767; Disease_resist.
DR InterPro: IPR002182; NB-ARC.
DR InterPro: IPR003880; Phosphopant_attach.
DR Pfam; PF00931; NB-ARC; 1.
DR PRINTS; PR00364; DISEASERISIT.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
DR PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
SQ SEQUENCE 1255 AA; 144354 MW; DF923D28BC7FEE6F CRC64;

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Query Match 18.1%; Score 852.5; DB 10; Length 1255;  
Best Local Similarity 30.1%; Pred. No. 1.1e-48;  
Matches 274; Conservative 156; Mismatches 336; Indels 145; Gaps 34;

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QY 31 REELALREKVSLEVFVKFEK---NNVFGEMTDFEVEYREVASAETITQLRLTGTV- 86
DB 413 KEIEELVKQDLKIFRSFFDAEQKYLDMARVLDVAEAKDVID-----SIIVRNGILH 468
QY 87 ----LGENKSQKKARRRPROSLOQVAEDMDHIMWKESTKIQDGKOVSKESLHDFSSST 142
DB 469 LIFSLPTITTKIKLILKEISALDENIPKDKGLIVNSPK-----KPERKSLTVD----- 518
QY 143 NDLKYNKNNVGRDQKOLLEDLRSYSGEPKVIDYVNGGIGTKTTLAKVYNDSEIIC 202
DB 519 ----KI---TVGEFEETNLILRLKT--SGSADLDVISTGHPGSGKTTIARKVYNSDNIVS 570
QY 203 REDVHAMATISQOHNKEKILLGLHSTIKMDRVKMIGEAELADMOKSLKRRYIIVLD 262
DB 571 RFDLRAMCTVQDCDEK--LANTIFSOVS--DSDSKLSENIADVADKLRLKQLFGKRYIIVLD 628
QY 263 DIMSCVMDGVRCFPTEDNAGSRILLTTRNDNVACYAGVENSLRMSFMDQESW 322
DB 629 DVMDDTTWELTTRPP--ESKSGSRITLTTRREKVALAHGKLNDDPLDRLRLPDESHELL 667
QY 323 SAFSSEALPYEFETVQKQIADCHGLPLTIVVAGIL---KSKRTIEDMKTAVAKDVKSP 379

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Db 688 KRAFGNESCPELDLVGKEIAENCKGLPIVADLIAGIAGREKKRSY--WLEVOSSLSF 745  
 QY 380 VTNDPDRCSRVGLSDHILTSIDKTCCLHFGIPEPDSIPVKNLMRSMMAEGL-KLE- 437  
 Db 746 ILNSEVE-VNKKYIELSDYDHPHKLPCCLYFASFPRKDTSLTIELVNYFGAEFVKTEM 804  
 QY 438 NDEGEVEKCLQELVDCVLSYKRSRDKIKSCAKVHDILYLCAREVORENIFI---- 493  
 Db 805 NSMEEVKTIYMDLILYSLVICF--NEIGYAL-NFQIHDLVHPCLIKAKKEMLPQINS 861  
 QY 494 -----MNDIVLVSYEPCSYLCKMOPKRYTGDINTCPYG 531  
 Db 862 SAPSDDLPROITIDCEEHGGLNFWFDSNKKRSGKHLYSL-----RIIGD----- 909  
 QY 532 LYRALLPVRQLDHNHNNLLKRTSHVSFPHLEPLYYVLAKSEVYHKLKLYELKHQI 591  
 Db 910 -----QDDSVSD-----AFHNR-----HRLRLVLDLHRTSFI 937  
 QY 592 ---DGFPEILSLIMLRYLSLSYGNEDVPPEICRLMNIQTIVQRPESDIIFAEIWE 648  
 Db 938 MYKSSLNEICMLNHLRYLSIDYQVK-LPLSFSNLMNLESLEYSTRS-ILVLLRRIID 995  
 QY 649 LMQLRHKLKP--RFLPDGSGSYDKGRHLDPSNLOTISYL--SPRCCTEYVIMGIQNVK 704  
 Db 996 LVKRLRYLSDVACSEFMDADE-SILLIADYKLENLRLITELLISYKDTKNIKRREPNDQ 1054  
 QY 705 KLGISGNKDDYKSPRDSGLPNNLVYLQLELLISVDYLLPVIISAKA----- 755  
 Db 1055 LLSFE-LKESWDYSTEQHWSELDLFELETL---SYGFSSNTNDSGSSVAINRRPDIH 1110  
 QY 756 FPAFLIKLKLERYLSMSYLDIIAELPNLEVLKIMDACCCEEMHPIVMG---FNRKL 811  
 Db 1111 FPMKLITLMIREPLTSDSLSTARLPNLELSLYHTIIGSEWN--MGEDPTFEMLK 1167  
 QY 812 LLITSLKLFMKKANDPNVLERIMISCKNLKEIPLEFDIHTILOLEHRECPKIGES 871  
 Db 1168 LNFQVSIKRWEGSEFPLEKIKLGRCHLEIPSEFDIYSLKSITIKV--SPOLEDS 1226  
 QY 872 AARIQKQEDL 882  
 Db 1227 ALKITEVAEDM 1237  
 RESULT 13  
 094107 PRELIMINARY; PRT; 1271 AA.  
 AC 094107;  
 DT 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE TOSPOVIRUS RESISTANCE PROTEIN C.  
 OS SMS-C.  
 OS Lycopersicon esculentum (Tomato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Eudicotyledons; core eudicots;  
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.  
 OX NCBI\_Taxid=4081;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. STEVENS;  
 RA Folkeetsma R.T., Spassova M.I., Prins M., Stevens M.R., Hille J.,  
 RT "Construction of a bacterial artificial chromosome (BAC) library of  
 RT Lycopersicon esculentum cv. Stevens and its application to physically  
 RT map the Sw-5 locus";  
 RL Mol. Breed. 5:197-207(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. STEVENS;  
 RA Prins T.W., Spassova M.I., Prins M., Klein Lankhorst R.,  
 RA Folkeetsma R.T., Hille J., Goldbach R.W.;  
 RT "The Sw-5 locus confers resistance to Tospoviruses";  
 RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY007367; AAC31015.1; "-"  
 SQ SEQUENCE 1271 AA; 147392 MW; 07D43B369C34E001 CRC64;  
 Query Match 18.0%, Score 849.5; DB 10; Length 1271;  
 Best Local Similarity 27.6%; Pred. No. 1.8e-48;  
 Matches 279; Conservative 184; Mismatches 324; Indels 223; Gaps 41;  
 QY 4 ASVASLMRTIESLLFNFSMOSLSODHRE--LCALR--EYVSSLEVYVKNKFNKNNV- 57  
 Db 336 AAGDVLYYIOKL-----LSIKKDNDSKISLSIQIMWETKDKLAQVETVYSKFTP 390  
 QY 58 -----GEMTDEVEVREY-----ASAAYTI-----QLRTGTVLGENKSKOKK 96  
 Db 391 SQFPYVGGSFIDSLIRKLEKMSKSKSCLDFIMKRLGNLEKLSIQISLEKDS----- 446  
 QY 97 ARRRFROSLQOVAEDMDHIMESTKIQDKK-----QVSKESLV-----HDESS 140  
 Db 447 -----SLSSILRDVAVKHHEHILODLRRTIMAYEAEAIAISILAQYVFWHIFCS 499  
 QY 141 STNDILKVK-----NNMYGRDQQRKOL 162  
 Db 500 LPTILKEIKQIVQYQKMSADIALKPCYVVAPEFFPTPHNINPTDIDYVGFQNDIEKM 559  
 QY 163 LBDLTRSYSGEPRVPIPVGMGIGTTLAKEVYNDESILCRFDYHAMATISQAHNKKEL 222  
 Db 560 FQYLIRG--INDIDIVPYGMGOGKTVAARKYNSDNIVSHFDVRAWCIVSQYVRRKLL 618  
 QY 223 LGLHSTIKMDRVKMGIAELADMLQKSIKRRRLVLDIOWSEVNDVGRRCPTEDN 282  
 Db 619 OELISQVTSKD--RGYEDDILADELRKSLMGKRLIILDDMDQMDAMDRLSLFSDSGN 676  
 QY 283 ACSRIILTRT-----NDEVACYAGVENFSLRMSFMDQDESSWLSFKSAFSSALPYEFETV 338  
 Db 677 R-SRIVYTRLEKVGEOVKCH--TDPSYL--PELKESCELLQKVKYQKEDFPELODV 731  
 QY 339 GKQIADDECHGLPITYVAVAGLLKSKRTIEDKTKYAKDVKSFYTPNDPDRCSR-VLGLSYD 397  
 Db 732 SOAVAKCKGGLPVLIVLVAGIILKRRMESWNNELKDLFYLIDCHSQYRARVQQLSFD 791  
 QY 398 HLTSIDKTCCLHFGIPEPDSIPVKNLMRSMMAEGLLENDLEGEVKECQELVDRCV 457  
 Db 792 NLADCLKPCLLYMGMPEDASIIVSALSLMTAEDFVO---NIE-SADYTLMLNLSNVV 847  
 QY 458 LVKRSRDSGTIKRSCKVHDILYLCAREVORENIFIM-----NDIVLVSYEPCSYL 509  
 Db 848 MYSKKEYNG-KIKYCKVHYVHLPCLEKSRRENFVAKGNHSGOPQVYMGOS--RVSFS 904  
 QY 510 CMYKMQPFRVYTGDEINCCPYGLYRALLTPVNRQLRDHNNLLKRTSHVSFPHLEPLY 569  
 Db 905 LSEENKRFASKT-----RKCSHQPLRLSLIT-----NGASFIDTISL- 939  
 QY 570 VLKSEVYH-FKLKYLELHRQIDGF-----PREILSLIMLRYLSLSYGNEDVPPEIC 622  
 Db 940 ---SSLIHRLRLKLVVLSHVEDVYNSATLKPMLWLYLGVASTFY---FD---RES 989  
 QY 623 RLMLNQTIVQRPESDIIFAEIWEIMQLRHKLPRFYLDPDPSGSYDK--GRHLDFSNL 681  
 Db 990 HLPHELETLIVKNNRS--VNLRCGFMEQGLRHVEL-----SDAERDKQGLFGSGSKL 1039  
 QY 682 QTIYSLSPRCCTKEYVIMGIQNVKKGIGSNKDDYKSFSDSGLPNNLVYLQOLET----- 735  
 Db 1040 ENMLRL-----KNI--VGFPIDRADVYSRR--CPN---LQDLHIEFEYFA 1077  
 QY 736 -----LSLISVDYSLPVIISAKAFPATIKKLKLERTYLSMSYLDIIAELPN 783  
 Db 1078 EPPFWLTGLNLTQDLIDLSFRLSHW--SGDLPENLMLVLRADLE-KLTSFYAGLPS 1134  
 QY 784 LEVLKIMDACCCEEMHPIVMGFNRLKLLIKYSLKFMKATNDFPVLERIMISCKNL 843  
 Db 1135 LEVLTQNTMYRFSQSEMCGLDIFHFKIKLLKLVQDLISMDVSESEFPLELIIIRMCNLT 1194  
 QY 844 KEIPLEFADIHITLOLEHRECPK-LGESARIQKE-QEDLGNNPVDVRI 891

DB 1195 EEPISFADVPILKQIKLHCKKSLDSDSAVRKIKDVEENEGNDRIDLI 1244

## RESULT 14

ID 094106 PRELIMINARY; PRT: 1263 AA.

AC 094106;  
 DT 01-DEC-2001 (TREMblrel. 19, Created)  
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE TOSPOVIRUS RESISTANCE PROTEIN D.  
 GN SWS-D.  
 OS Lycopersicon esculentum (Tomato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 CC Asteridae; eusterids I; Solanales; Solanaceae; Solanum.  
 CX NCBI\_TaxID=4081;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. STEVENS;  
 RA Folterisma R.T., Spassova M.I., Prins M., Stevens M.R., Hille J.,  
 RA Goldbach R.W.;  
 RT "Construction of a bacterial artificial chromosome (BAC) library of  
 RT Lycopersicon esculentum cv. Stevens and its application to physically  
 RT map the Sw-5 locus."  
 RL Mol. Breed. 5:197-207(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. STEVENS;  
 RA Prins T.W., Spassova M.I., Prins M., Klein Lankhorst R.,  
 RA Folterisma R.T., Hille J., Goldbach R.W.;  
 RT "The Sw-5 locus confers resistance to Tospoviruses."  
 RT Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY007367; AAC31016.1;  
 SQ SEQUENCE 1263 AA; 146026 MW; D3275C734BE358AD CRC64;

Query Match 18.0%; Score 848.5; DB 10; Length 1263;  
 Best Local Similarity 29.1%; Pred. No. 2.1e-48;  
 Matches 278; Conservative 168; Mismatches 331; Indels 177; Gaps 38;

QY 8 SLMRT-----ESLTFNSPMQSLCDHRE-----LCALREKYSLEFVFNKKNVGE 59  
 DB 391 SLIRKLNEMSRKSGYDFLAKPFCLEKQSLINLKEKLSLSIRDTYK--VHNE 448  
 QY 60 MTD-----FEVEVREVASAEYTIQLRL--TGIVLGENKSOKKARRRFRSL-- 105  
 DB 449 OKDQGRRTINLAVGVSIDSICAKYVFWHCFCSPLTLEIKQINAEVTEWMSADIP 508  
 QY 106 --QVAEDMDHI--WKSTKIQK-----GKQVSKESLHDFSSSTNDILKKNMVG 154  
 DB 509 NPHYVAAPKHLPTRHSDNITDEIYDEIVGIDKEKTIQCVIRGTNDL----- 559  
 QY 155 RDOQRKQLLEDLRSYSGEPKVIPIVGMGIGIKTKLAKEYYNDSEILCFEDVHAMATISQ 214  
 DB 560 -----DVPVIVGMGGGKTTIARAYVNSDNIIVSHEDVAMQVISO 599  
 QY 215 QHNKKEIILGLHSTIKMDRYKMGCEALADMOKSLKRRKLYLVIDIWSEVWDGVR 274  
 DB 600 TYRRKRLIQIISQVYGRD--KGVEDDILADELRKSLMKRRLYLIDDMWDMAMDRLR 657  
 QY 275 RCPPTEDMNGSRILLTTR-----NDEVACYAGVNFSLRMSFMDQDSWSLFRSAFSSSA 330  
 DB 658 LSPFDGGR-SRIIVTTRLEKGEQVCH--IDPYSL--PELTTESSKILLQKVKOKED 712  
 QY 331 LPEFETVQKQADECHGLPLTIVVAGLLKSKRTIEDMTKVAQ--VKSEFTNDPDERCS 389  
 DB 713 CPPELDQVSVNAEKCKGLPLVIVLAGITKKRMESSWDELDRSLFDYLDCHSEQYSL 772  
 QY 390 RVLGSLSYDHLTSLKTKCLAHFGIFPPDSIDPIVKNLMRSNMAAGFKLKLDEBEVEVCIO 449  
 DB 773 ATMQLSFDNLADCLPKCLLYMGFPEDASINVSALLSLWIAEDFVQ--NIE--SAEDYLM 828

QY 450 ELYDRCIVLYSKRSRDGFTIRSCKYHDLIYDLCVREVOENEFIM--NDIYLDVSYPEC 506  
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 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
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 OS Lycopersicon esculentum (Tomato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
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 RA Rossi M., Goggin F.L., Milligan S.B., Kaloshian I., Ullman D.E.,  
 RA Williamson V.M.;  
 RT "The nematode resistance gene M1 of tomato confers resistance against  
 RT the potato aphid."  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:9750-9754(1998).  
 RN [2]  
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 RC STRAIN=CV. MOTELLE;  
 RA Bodeau J.P., Kaloshian I., Milligan S., Williamson V.M.;  
 RT "Isolation and large-scale sequencing of bacterial artificial  
 RT chromosomes (BACs) spanning the tomato M1 nematode-resistance  
 RT locus."  
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U81378; AAC32252.1;  
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Query Match 17.7%; Score 834.5; DB 10; Length 1206;





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GenCore version 4.5  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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## ALIGNMENTS

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DEFINITION Sequence 4 from Patent WO0107635.  
ACCESSION AX076883  
VERSION AX076883.1 GI:13121544  
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SOURCE Capsicum annuum.  
ORGANISM Capsicum annuum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asteridae; euasterids I; Solanales; Solanaceae; Capsicum.

REFERENCE 1 (bases 1 to 2718)  
AUTHORS Staskiewicz,B.J., Dahlbeck,D. and Tai,T.H.  
TITLE Bst2 resistance gene  
JOURNAL Patent: WO 0107635-A 4 01-FEB-2001;  
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)  
LOCATION/Qualifiers  
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Query Match 100.0%; Score 2718; DB 6; Length 2718;  
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SOURCE Capsicum annuum.  
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 REFERENCE  
 AUTHORS Staskiewicz, B.J., Dahlbeck, D. and Rai, T.H.  
 TITLE B22 resistance gene  
 JOURNAL Patent: WO 0107635-A 2 01-FEB-2001;  
 THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)  
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FEATURES	source
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Dd	93	ATGGCTCATGTCAAGTGTGCGTCTCTTTATGAGAACAATAATGAATTCCTTGACATTCAT	152							
OY	61	tgcgcgatgcaatctcttatccctgtatcacagaagaactttggctctcttgttaaaaa	120							
Dd	153	TGCGCGATGCCAATTCCTATCCGTGTATCCACAGAAAGAACTTTGGCGCTTGTGTGAAAA	212							
OY	121	gttagttcccctggaagatttttgaaagacctttggaanaaacatagtttttgggaaaty	180							
Dd	213	GTTAGTTCCCCTGGAAGTATTTTTCAAGAACCTTTGAGAAAAACAATGTTTTTGGGAAAAG	272							
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Dd	393	TTTTGCTCAAAGCCTGCACAAAGTAGCACAGGACATGAGCATATCTGGAAAAAGTCGACA	452							
OY	361	aagatccaagataaagaagaaacaaglatlacaagaagatcaltgttcaatgattttcaagt	420							
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Dd	633	GGGATGGGAGCGCATAGGTAAACAACTTAGCAAAAAGAAATTACATGATGATCAATCAANT	692							
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Dd	813	GAAAGAGAGCTTAGACACATGTTACAGAAAAATTAAAGAGAAAGAGTACTAATTGTGC	872							
OY	761	ttggaatgatcttggagtttgyaagltgyggaatggcgtlgagacgatalgcttccaaatgaa	840							
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 ACCESSION AX076880  
 VERSION AX076880.1 GI:13121541  
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 ORGANISM Capsicum annuum  
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Asteridae; euasterids I; Solanales; Solanaceae; Capsicum.  
 REFERENCE 1 (bases 1 to 31491)  
 AUTHORS Staskiewicz, B.J., Dahlbeck, D., and Tai, T.H.  
 TITLE B2 resistance gene  
 JOURNAL Patent: WO 0107635-A 1 01-FEB-2001;  
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ACCESSION	AJ249449				
VERSION	AJ249449.1	GI:5911744			
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SOURCE	potato.				
ORGANISM	Solanum tuberosum				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.				
AUTHORS	1 (bases 1 to 3254)				
TITLE	Bendahmane, A., Querol, M., Kanyuka, K. and Baulcombe, D.C. Agrobacterium transient expression system as a tool for the isolation of disease resistance genes: application to the Rx2 locus in potato				
JOURNAL	Plant J. 21 (1), 73-81 (2000)				
MEDLINE	20117531				
REFERENCE	2 (bases 1 to 3254)				
AUTHORS	Bendahmane, A.				
TITLE	Direct Submission				
JOURNAL	Submitted (13-SEP-1999) Bendahmane A., Salisbury Laboratory, John Innes Center, Colney Lane, Norwich NR4 7UH, UNITED KINGDOM				
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 REFERENCE 1 (bases 1 to 10331)  
 AUTHORS Van der Vossen, E.A.G.  
 TITLES Direct Submission  
 JOURNAL Submitted (19-OCT-1999) Genomics, CPRO, Droeendaalsesteeg 1,  
 Wageningen 6708 PB, The Netherlands

FEATURES  
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BASE COUNT 3150 a 1342 c 1924 g 3714 t 1 others

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RESULT 10  
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DEFINITION Sequence 12 from Patent W09954490.  
ACCESSION AX012617  
VERSION AX012617.1 GI:9998601  
KEYWORDS  
SOURCE potato.  
ORGANISM Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.  
REFERENCE  
1 (bases 1 to 3229)  
Baulcombe, D.C., Bendahmane, A. and Kanyuka, K.V.  
Plant-derived resistance gene  
Patent: WO 9854490-A 12-28-OCT-1999.  
AUTHORS BAULCOMBE DAVID CHARLES (GB); BENDAHMANE ABDELHAFID (GB); KANYUKA  
JOURNAL KONSTANTIN VALERIEVICH (GB); PLANT BIOSCIENCE LIMITED (GB)  
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Query Match 10.0%; Score 272.4; DB 6; Length 3229;  
Best Local Similarity 55.0%; Pred. No. 1.6e-53;  
Matches 728; Conservative 0; Mismatches 551; Indels 45; Gaps 8;

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DEFINITION Sequence 13 from Patent W09954490.  
ACCESSION AX012618  
VERSION AX012618.1 GI:9998602  
KEYWORDS  
SOURCE potato.  
ORGANISM Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;



REFERENCE 1 (bases 1 to 3229)  
 AUTHORS Baulcombe, D.C., Bendahmane, A. and Kanyuka, K.V.  
 TITLE Plant-derived resistance gene  
 JOURNAL Patent: WO 9954490-A 13 28-OCT-1999;  
 BAULCOMBE DAVID CHARLES (GB); BENDAHMANE ABDELHAFID (GB); KANYUKA KONSTANTIN VALERIEVICH (GB); PLANT BIOSCIENCE LIMITED (GB)  
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 VERSION AJ249448.1 GI:5918253  
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 RX2.ac15 gene.  
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 ORGANISM Solanum acule.  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum.  
 REFERENCE 1 (bases 1 to 3229)  
 AUTHORS Bendahmane, A., Querici, M., Kanyuka, K. and Baulcombe, D.C.  
 TITLE Agrobacterium transient expression system as a tool for the  
 isolation of disease resistance genes: application to the Rx2 locus  
 in potato.  
 JOURNAL Plant J. 21 (1), 73-81 (2000)  
 MEDLINE 20117531  
 REFERENCE 2 (bases 1 to 3229)  
 AUTHORS Bendahmane, A.  
 TITLE Direct Submission  
 JOURNAL Submitted (13-SEP-1999) Bendahmane A., Sainsbury Laboratory, John  
 Innes Center, Colney Lane, Norwich NR4 7UH, UNITED KINGDOM  
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 VERSION AX012614.1 GI:9998598  
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 Asteridae; euasterids I; Solanales; Solanaceae; Solanum.  
 REFERENCE 1 (bases 1 to 3220)  
 AUTHORS Baulcombe, D.C., Bendahmane, A. and Kanyuka, K.V.  
 TITLE Plant-derived resistance gene  
 JOURNAL Patent: WO 95/4490-A 9 28-OCT-1999;  
 BAILCOMBE DAVID CHARLES (GB); BENDAHMANE ABDELHAFFID (GB); KANYUKA  
 KONSTANTIN VALERIEVICH (GB); PLANT BIOSCIENCE LIMITED (GB)  
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 REFERENCE 1 (bases 1 to 5820)  
 AUTHORS Baulcombe, D.C., Bendahmane, A. and Kanyuka, K.V.  
 TITLE Plant-derived resistance gene  
 JOURNAL Patent: WO 9954490-A 1 28-OCT-1999;  
 BAULCOMBE DAVID CHARLES (GB); BENDAHMANE ABDELHAFFID (GB); KANYUKA  
 KONSTANTIN VALERIEVICH (GB); PLANT BIOSCIENCE LIMITED (GB)  
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 KEYWORDS potato.



JOURNAL Plant Cell 11 (5), 781-792 (1999)  
 MEDLINE 9264301  
 REFERENCE 2 (bases 1 to 18284)  
 AUTHORS Bendahmane, A.  
 TITLE Direct Submission  
 JOURNAL Submitted (03-AUG-1998) Bendahmane A., The Sainsbury Laboratory,  
 John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk  
 NR4 7QH, United Kingdom

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 IDSTVKQWMAITSDSKDKLPOTSLSVSPEDVQPEINMGRENEEMLDJLARG  
 RELEVSVIVGSGIGKTTLAIRKIVSDPCIMSRTFIDKATVSDCYRANVLLGLSLT  
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 VAEYASGKPEHMRNMNDESNLHLKRIPEKGSYSEPEINIKOIALKCGGLPIA  
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 IDRGCTAPRLLIPPPAPRONKSLTFPFGSAWMDISVGLKPLREVLITSMNF  
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BASE COUNT 5967 a 3022 c 3120 g 6175 t  
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Query Match 10.0%; Score 271.6; DB 8; Length 18284;  
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 Db 11961 TGGAGAAATCTGCAATTAATGAGGCGATGAGAGGGTTTAACAATCTTGGAAAGTTGAAA 12020  
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QY 200 taagaagatttgcagtgctgtgatacacaaactcaactgagactacaggaactgttac 259  
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QY 380 aacaagtaacaagaatcatgtgtcatgatttttcaagttcaacaacagatatttga 439  
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Db 12201 AAGATCTAAACCAACCAACTAGCTGCTTGTCACTTTACCTG---AACATGATGTTGAGC 12257  
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Db 12258 ACCCCGAGAAATTAATGTTGGCCCGTGAAAATTTGATGATGATGCTGATCAACTTG 12317  
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QY 500 ctgagaagcactctggggaaccacaagatcatccgatttcgggagtgagagcatagta 559  
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QY 560 aaacaaccttagcaaaagaagtttacaatgatgatcaatctatgacgttttagatgtc 619  
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QY 740 tgttacagaaagaagtttaagaagaagagtagtaattgtcttgatgtagatctgagatt 799  
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QY 800 gtgaagtgtaggaatgagcgtgtagaagcagatcttccaaactgaagaacaatgcaagagtcgaa 859  
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Db 12594 CAGAAGCTTGGATGATTAATAAACTATGTTCCCA---GACTGTTAATAATGGAAGCAGAA 12650  
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QY 1154 atgaacgatgttcacgtgtgtgtgtgagttgaagatcaacttgcagacgatactaaaaa 1213  
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Db 13011 CGTGTTCCTGTATTTTGTGAATTTTACAGAGAGATGAACAGATTTCTGTAATTAAGACTTG 13070  
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QY 1274 tgaagatcatgtagtgcgtgaggggttcctga-----agttggaanaatgatttgaagag 1327  
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Db 13071 TTGAGTTATGCGCTGTAGAGGATTTTGTGAATGAAGAAGAGGAAACATAGAAAGAG 13130  
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QY 1328 aggttgagaagtggttgcagaagcctgtgcagatagatgtctcctgtgcagaagagaa 1387  
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Db 13131 TGGCAACAACATGTATTAACGAACTTATAGATGAGAAGCTTAATTTTCAACCAATTTTA 13190  
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QY 1388 gtccgagatggaacaaaatagatcatcatgtaaggttcaatcatatataatgacccgtgtgc 1447  
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Db 13191 GTTTTCGTGGAACATAGAAAG---TTGTGGAATGATATGTGACCCCTGGAATCTGT 13247  
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QY 1448 tgaagaagttcaaggggagacattttaa---taatgaagacattgttcttgcagtat 1504  
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Db 13248 TGAGGGAAGCTCGAAGATGATTTTGTGAATGTTATCAGAGAAAGAGTGTCAAAATTT 13307  
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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 11, 2002, 22:37:03 ; Search time 881.41 Seconds  
(without alignments)  
5294.441 Million cell updates/sec

Title: US-09-864-680-4

Perfect score: 2718  
Sequence: 1 atggtcctgcgaagtgtgc.....ctgattcagaagaacattag 2718

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

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23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.\*  
24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.\*  
25: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2718	100.0	2718	22	AA6F3303
2	2718	100.0	3099	22	ABD10204
3	2718	100.0	3099	22	AA6F3302
4	2685.6	98.8	31491	22	AA6F3303
5	2685.6	98.8	31491	22	AA6F3302
6	272.8	10.0	2739	21	AA502651
7	272.8	10.0	2817	21	AA502652
8	272.8	10.0	3683	22	AA503713
9	272.8	10.0	10329	21	AA502654

10	272.8	10.0	10329	21	AA505653	Genomic DNA encodi
11	271.6	10.0	5820	20	AA237153	DNA sequence of BA
12	269.6	9.9	3066	20	AA237154	Partial nucleotide
13	268	9.9	3014	22	AA503715	DNA encoding Rx 72
14	266.4	9.8	2880	22	AA503717	DNA encoding Rx 19
15	266	9.8	2885	22	AA503719	DNA encoding Rx 32
16	264.8	9.7	3283	22	AA503716	DNA encoding Rx 39
17	256.8	9.4	2679	22	AA503718	DNA encoding Rx 7,
18	172.2	6.3	5475	19	AA503717	Tomato Prf cDNA.
19	170	6.3	10968	19	AA503718	Tomato Prf genomic
20	149.2	5.5	3997	19	AA503719	Tomato Prf resist
21	149.2	5.5	9870	19	AA503720	Tomato Prf resist
22	149.2	5.5	9870	19	AA503721	Tomato Prf resist
23	149.2	5.5	51952	19	AA503722	Tomato Prf resist
24	147.6	5.4	3982	19	AA503723	Tomato Prf resist
25	132.2	4.9	23670	24	ABA97078	Tomato Hero gene c
26	119	4.4	3909	24	ABA97078	Tomato Hero gene A
27	103.4	3.8	534	21	AA51888	N. tabacum Class I
28	95.2	3.5	540	21	AA51891	N. tabacum Class I
29	94.4	3.5	3801	21	AA51892	N. tabacum Class I
30	94.4	3.5	6658	18	AA51893	N. tabacum Class I
31	92.2	3.4	532	21	AA51889	N. tabacum Class I
32	88.8	3.3	517	21	AA51884	N. tabacum Class I
33	83.6	3.1	4465	17	AA51835	I2C-2 gene encodin
34	81.4	3.0	477	21	AA51880	N. tabacum Enh8 ge
35	76	2.8	472	21	AA51876	N. tabacum Enh4 ge
36	74	2.7	644	21	AA51886	N. tabacum Class I
37	72.2	2.7	2862	21	AA51885	N. tabacum Class I
38	70.4	2.6	647	21	AA51899	Rice disease resist
39	66.6	2.5	489	21	AA51874	N. tabacum Enh2 ge
40	62.8	2.3	1028	21	AA51896	Rice disease resist
41	59.2	2.2	2954	21	AA51829	Sorghum resistance
42	59.2	2.2	6760	21	AA51823	Sorghum resistance
43	56	2.1	4948	17	AA51835	I2C-1 gene encodin
44	50.4	1.9	5910	19	AA51878	Rice bacterial lea
45	48.2	1.8	548	21	AAA40001	Rice disease resist

#### ALIGNMENTS

RESULT 1	
AA6F3303	AA6F3303 standard; cDNA; 2718 BP.
XX	
AC	AA6F3303;
XX	
02-MAY-2001	(first entry)
XX	
DE	Pepper Bs2 open reading frame sequence.
XX	
KW	Bs2; pepper; pathogen resistant; Xanthomonas campestris pv vesicatoria;
KW	Kcv; bacterial spot disease; transgenic plant; crop: fruit; flower; ss.
XX	
OS	Capsicum annuum.
XX	
PN	WO200107635-A1.
XX	
PD	01-FEB-2001.
XX	
PF	23-DEC-1999; 99WO-US30891.
XX	
PR	23-JUL-1999; 99US-0360186.
XX	
PA	(REGC ) UNIV CALIFORNIA.
XX	
PI	Staskawicz BJ, Dahlbeck D, Tai TH.
XX	
DR	WPI: 2001-168560/17.
XX	
PT	P-FSDB; AAB72198.
XX	
PT	Novel Bs2 polypeptide from Capsicum annuum for producing transgenic
XX	plants having resistance to bacterial spot disease caused by

PT Xanthomonas campestris pv vesicatoria (Xcv) -  
 XX Claim 3; Page 64-68; 72zp; English.

CC This invention relates to the amino acid sequence of the Bs2 protein  
 CC isolated from  *Capsicum annuum*  (pepper). The protein and DNA sequences of  
 CC Bs2 can be used to confer resistance to the plant pathogen  *Xanthomonas*   
 CC  *campestris*  pv  *vesicatoria*  (Xcv) which causes bacterial spot disease. Bs2  
 CC DNA and protein sequences are useful for producing transgenic plants such  
 CC as pepper, tomato, tobacco, broccoli, cauliflower, cabbage, canola,  
 CC cowpea, grape, bean soybean, rice, corn, wheat, barley, citrus, cotton,  
 CC cassava and walnut, having resistance to  *X. campestris* . The protein and  
 CC DNA molecule are also useful for producing transgenic alfalfa, flax,  
 CC sunflower, safflower, brassica, peanut, clover, lettuce, cucurbits,  
 CC potato, carrot, radish, pea, lentils, apples, pears, peaches, apricots,  
 CC carnations and roses having resistance to  *X. campestris* . The present  
 CC sequence represents the open reading frame of Bs2.

XX Sequence 2718 BP; 851 A; 454 C; 623 G; 790 T; 0 other;

# Query Match

100.0%; Score 2718; DB 22; Length 2718;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2718; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 atgctcatgcaagtgctgctctcttatgagaacaatagaatctcttgaattcaat 60  
 QY 61 tgcgcgatgcaatctctctctgctgatacagagaagaacttgcctctcgtagaaa 120  
 DB 61 tgcgcgatgcaatctctctctgctgatacagagaagaacttgcctctcgtagaaa 120  
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 DB 301 ttctgtcaaaagcctgcaaaagtagcagagacatgacatatactggaagaaagtcgaca 360  
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 DB 541 gggatgaggagatagtagtaaaacaacttagcaaaagaatttacaatgataatcaatt 600  
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 DB 601 ctatgcgcttttgatgttcaatgtcctggtgtacacatactcaacagcaacaacaaagga 660  
 QY 661 atttgcctggccttctgattccacaatcaaatggaatgagcagggttaagaattggt 720  
 DB 661 atttgcctggccttctgattccacaatcaaatggaatgagcagggttaagaattggt 720

QY 721 gaagcagagctagacagacatgtttacagaaaagtttaagaagaagagctaatgttc 780  
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Db 2701 gattcagaagaacattag 2718

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RESULT 2
AADI0204
ID AADI0204 standard; cDNA; 3099 BP.
XX
AC AADI0204;
XX
DT 24-SEP-2001 (first entry)
XX
DE Pepper Bs2 cDNA.

```

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XX Bs2 gene; pepper; resistance gene; plant pathogen; virulence gene;
KW bacterial spot disease; Xanthomonas campestris pv. vesicatoria;
KW AvrBs2; hypersensitive response; transgenic plant; tomato; tobacco;
KW rice; corn; wheat; ss.
XX Capsicum annuum.
OS
XX Key Location/Qualifiers
FH 93..2810
FT /*tag=a
FT /product= "Bs2 protein"
FT /note= "This region is claimed as SEQ ID NO:4
FT in claim 7"
XX
PN US6262343-B1.
XX
PD 17-JUL-2001.
XX
PE 23-JUL-1999; 99US-0360186.
XX
PR 23-JUL-1998; 98US-0093957.
XX
PA (REGC ) UNIV CALIFORNIA.
PI Staskawicz BJ, Dahlbeck D, Tai TH;
XX
DR WPI: 2001-450496/48.
DR P-PSDB: AAE05409.
XX
PT Nucleic acid molecules encoding Bs2 protein, useful for producing
PT transgenic plants having resistance to the plant pathogen Xanthomonas
PT campestris -
PT
PS Claim 7; Column 49-56; 37pp; English.
XX
XX The present sequence is Bs2 cDNA from pepper. The Bs2 gene is shown
CC to confer resistance to plant pathogen
CC Xanthomonas campestris pv. vesicatoria which causes bacterial spot
CC disease. The Bs2 protein has B2 biological activity, i.e., when
CC co-expressed in a plant with a X. campestris AvrBs2 gene product,
CC it produces a localised hypersensitive response. The protein
CC includes a nucleotide binding motif and leucine rich repeats of the
CC type found in other plant resistance genes. The Bs2 nucleic acid
CC molecule is useful for producing transgenic plants such as pepper,
CC tomato, tobacco, broccoli, cauliflower, cabbage, cowpea, grape, canola,
CC bean, soybean, rice, corn, wheat, barley, cotton, cassava and
CC walnut, that are resistant to plant pathogen Xanthomonas campestris.
CC The transgenic plants produced using Bs2 molecule develop a
CC hypersensitive response to the pathogen at the site of inoculation and
CC show an enhanced resistance to systemic infection. The Bs2 nucleic acid
CC molecule is also useful as polymerase chain reaction (PCR) primers for
CC amplifying portions of Bs2 nucleic acid molecule, as sequencing primers
CC to verify the authenticity of an amplified molecule, and as
CC hybridisation probes.
XX
XX Sequence 3099 BP; 970 A; 514 C; 693 G; 922 T; 0 other;
SQ

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Query Match 100.0%; Score 2718; DB 22; Length 3099;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2718; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 tcgcgatgcaatctctatctctgtgacacagagaagaattggcgtctctgtgaaaa 120
Db 153 tcgcgatgcaatctctatctctgtgacacagagaagaattggcgtctctgtgaaaa 212
QY 121 gttagttccttggaaggtattgttcaagaactttgagaagaacaattgttttggaatg 180

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 Db 2793 gattcagaagaacattag 2810

## RESULT 3

AAAF63302 standard; CDNA; 3099 BP.

ID AAF63302;

AC AAF63302; (first entry)

XX 02-MAY-2001

XX 02-MAY-2001 (first entry)

XX 02-MAY-2001 (first entry)

XX 02-MAY-2001 (first entry)

XX 02-MAY-2001 (first entry)

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XX 02-MAY-2001 (first entry)

XX 02-MAY-2001 (first entry)

XX 02-MAY-2001 (first entry)

XX 02-MAY-2001 (first entry)

CC DNA molecule are also useful for producing transgenic alfalfa, flax,  
 sunflower, safflower, brassica, peanut, clover, lettuce, cucurbits,  
 potato, carrot, radish, pea, lentils, apples, pears, peaches, apricots,  
 carnations and roses having resistance to X. campestris. The present  
 CC sequence represents CDNA encoding Bs2.  
 CC  
 XX Sequence 3099 BP; 970 A; 514 C; 693 G; 922 T; 0 other;

Query Match 100.0%; Score 2718; DB 22; Length 3099;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2718; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 atggtctcagcagagtgctgtctctctatgagacataatgactctctgacatcaat 60  
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 Db 153 tcgcatgcatctctatctctgtgatacagagaacatttgctctctgtgaaaaa 212  
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QY 1801 ctcaatcgtgtgagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcag 1860
Db 1893 ctcaatcgtgtgagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcag 1952
QY 1861 atttgagatgtagaataatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcag 1920
Db 1953 atttgagatgtagaataatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcag 2012
QY 1921 atttgagatgtagaataatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcag 1980
Db 2013 atttgagatgtagaataatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcag 2072
QY 1981 tattgcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcag 2040

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Db 2073 tattgcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcag 2132
QY 2041 ttacaacatattcttactgtctccacagctgtgtgtagcagagagatgtagcagatgtagcagatgtagcag 2100
Db 2133 ttacaacatattcttactgtctccacagctgtgtgtagcagagagatgtagcagatgtagcagatgtagcag 2192
QY 2101 cagaatgtagaataatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcag 2160
Db 2193 cagaatgtagaataatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcag 2252
QY 2161 tcttgagcttcccaacatctgtctatctgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcag 2220
Db 2253 tcttgagcttcccaacatctgtctatctgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcag 2312
QY 2221 gtgtatataagccttctgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcag 2280
Db 2313 gtgtatataagccttctgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcag 2372
QY 2281 aagaagttgaagttgtagaagaacttataagctgtagcagatgtagcagatgtagcagatgtagcagatgtagcag 2340
Db 2373 aagaagttgaagttgtagaagaacttataagctgtagcagatgtagcagatgtagcagatgtagcagatgtagcag 2432
QY 2341 ttgccaacctgtagctgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcag 2400
Db 2433 ttgccaacctgtagctgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcag 2492
QY 2401 ccaatgtagttagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcag 2460
Db 2493 ccaatgtagttagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcag 2552
QY 2461 ttctggaagaagcacaatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcag 2520
Db 2553 ttctggaagaagcacaatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcag 2612
QY 2521 aaaaattgaaagaatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcag 2580
Db 2613 aaaaattgaaagaatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcag 2672
QY 2581 ttgaagaatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcag 2640
Db 2673 ttgaagaatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcag 2732
QY 2641 gacctggaagaagaacctgtgtagctgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcag 2700
Db 2733 gacctggaagaagaacctgtgtagctgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcag 2792
QY 2701 gattcagaagaacattag 2718
Db 2793 gattcagaagaacattag 2810

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RESULT 4
AADI0203 standard; DNA; 31491 BP.
XX
AC AADI0203;
XX
DT 24-SEP-2001 (first entry)
XX
DE Pepper Bs2 gene.
XX
KW Bs2 gene; pepper; resistance gene; plant pathogen; virulence gene;
KW bacterial spot disease; Xanthomonas campestris pv. vesicatoria;
KW AvrBs2; hypersensitive response; transgenic plant; tomato; tobacco;
KW rice; corn; wheat; ds.
XX
OS Capsicum annuum.
XX
XX Key location/Qualifiers
FH 1..502
FT promoter
FT exon 503..554

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[illegible]

Db	3640	tcctggctccccaacacatctctgtctacccgcagaacacttgaaacattgagcttatact	3699
Oy	2221	gttcatatagacctttgccaagtgatcatcttcaagtgcgaagagcttttcagacaagcttc	2280
Db	3700	gttgattatagcctctttgcagtgatcatcttcaagtgcgaagagcttttcagacaagcttc	3759
Oy	2281	aagaagttgaagttggaagaactctctaagctggtgcatactctggaatcatagctgag	2340
Db	3760	aagaagttgaagttggaagaactctctaagctggtgcatactctggaatcatagctgag	3819
Oy	2341	ttgcctaacttgagttgctcgaagctcgatgatacgctttgttggttggaagtggcat	2400
Db	3820	ttgcctaactctgaagtgctcgaagctcgatgatacgctttgttggttggaagtggcat	3879
Oy	2401	ccaattgttatgttgatcttaactgatgaaagctttgtccaatttaaatagtttctcaag	2460
Db	3880	ccaattgttatgttgatcttaactgatgaaagctttgtccaatttaaatagtttctcaag	3939
Oy	2461	tctctggaagaccaccaatgatacaatttctctgctcttgagcgccctcatgatgaaagttgc	2520
Db	3940	tctctggaagaccaccaatgatacaatttctctgctcttgagcgccctcatgatgaaagttgc	3999
Oy	2521	aaaaattggaagagatacccatgttgatgttgagataatacacacatacagctcgattgg	2580
Db	4000	aaaaattggaagagatacccatgttgatgttgagataatacacacatacagctcgattgg	4059
Oy	2581	ttaagaagagtgctctcccaactttggagatctgtctgcagaatttcagaagaagaacaa	2640
Db	4060	ttaagaagagtgctctcccaactttggagatctgtctgcagaatttcagaagaagaacaa	4119
Oy	2641	gactctggaacaacacctgtgagctgtctgatactcaataatcatctgaaagaga	2692
Db	4120	gactctggaacaacacctgtgagctgtctgatactcaataatcatctgaaagaga	4171
RESULT 5			
AAAF63301			
ID	AAF63301 standard; DNA; 31491 BP.		
XX			
AC	AAF63301;		
XX			
DT	02-MAY-2001 (first entry)		
XX			
DE	Pepper Bs2 resistance gene.		
XX			
KM	Bs2; pepper; pathogen resistant; Xanthomonas campestris pv vesicatoria;		
KW	Xcv; bacterial spot disease; transgenic plant; crop; fruit; flower; ds		
XX			
OS	Capsicum annuum.		
XX			
PN	WO200107635-A1.		
XX			
PD	01-FEB-2001.		
XX			
PF	23-DEC-1999; 99MO-US30891.		
XX			
PR	23-JUL-1999; 99US-0360186.		
XX			
PA	(REGC ) UNIV CALIFORNIA.		
XX			
PI	Staskawicz BJ, Dahlbeck D, Tai TH;		
XX			
DR	WPI: 2001-168560/17.		
XX			
DR	P-PSDB; AAB72198.		
XX			
PT	Novel Bs2 polypeptide from Capsicum annuum for producing transgenic		
XX	plants having resistance to bacterial spot disease caused by		
XX	Xanthomonas campestris pv vesicatoria (Xcv) -		
XX			
PS	Claim 3; Page 40-57; 72pp; English.		
CC	This invention relates to the amino acid sequence of the Bs2 protein		



isolated from  *Capsicum annuum*  (pepper). The protein and DNA sequences of B52 can be used to confer resistance to the plant pathogen  *Xanthomonas campestris pv vesicatoria*  (Xcv) which causes bacterial spot disease. B52 DNA and protein sequences are useful for producing transgenic plants such as pepper, tomato, tobacco, broccoli, cauliflower, cabbage, canola, cowpea, grape, bean soybean, rice, corn, wheat, barley, citrus, cotton, cassava and walnut, having resistance to  *X. campestris* . The protein and DNA molecule are also useful for producing transgenic alfalfa, flax, sunflower, safflower, brassica, peanut, clover, lettuce, cucurbit, potato, carrot, radish, pea, lentils, apples, pears, peaches, apricots, carnations and roses having resistance to  *X. campestris* . The present sequence represents the B52 gene of the invention.

Sequence 31491 BP; 9652 A; 6345 C; 5992 G; 9502 T; 0 other;

Query Match 98.8%; Score 2685.6; DB 22; Length 31491;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2688; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 atggtctatgcaagtggtgctctcttattgataacaatgaatctcttgcattcaat 60  
DB 1480 atggtctatgcaagtggtgctctcttattgataacaatgaatctcttgcattcaat 1539  
QY 61 tcgcgatgcaatctctatcctctgatacacagaaagaacttgcgctcttcgtgaaaa 120  
DB 1540 tcgcgatgcaatctctatcctctgatacacagaaagaacttgcgctcttcgtgaaaa 1599  
QY 121 gttatgtcccttggaaagtatttgcagaactttgagaaaaaactgttttggggaatg 180  
DB 1600 gttatgtcccttggaaagtatttgcagaactttgagaaaaaactgttttggggaatg 1659  
QY 181 agggatttgaagtgaagtaagaagaagtgcagtcgctgcgaataaccaattcaacg 240  
DB 1660 agggatttgaagtgaagtaagaagaagtgcagtcgctgcgaataaccaattcaacg 1719  
QY 241 agacttaacagaaactgtactctggagaaaaataaagccagaaaaaagcgctgcaag 300  
DB 1720 agacttaacagaaactgtactctggagaaaaataaagccagaaaaaagcgctgcaag 1779  
QY 301 ttctgtcaaacgctgcacaagaatgacagagacatgatactctgaaaaagatcgaca 360  
DB 1780 ttctgtcaaacgctgcacaagaatgacagagacatgatactctgaaaaagatcgaca 1839  
QY 361 aagatccaagataaagaagaacaagaatatacaagaatctgttataatttttaagt 420  
DB 1840 aagatccaagataaagaagaacaagaatatacaagaatctgttataatttttaagt 1899  
QY 421 tcaacaacagatatttgaaggtttaagaacaatatgttgcacgttgatcaagaagaa 480  
DB 1900 tcaacaacagatatttgaaggtttaagaacaatatgttgcacgttgatcaagaagaa 1959  
QY 481 caagtgttaagaagatctgactagaagctactctggggaacccaagtcaccgattgtc 540  
DB 1960 caagtgttaagaagatctgactagaagctactctggggaacccaagtcaccgattgtc 2019  
QY 541 gggatggggagagataaggttaaaaaaaccttagcaaaaagaagtttacaatattgaataat 600  
DB 2020 gggatggggagagataaggttaaaaaaaccttagcaaaaagaagtttacaatattgaataat 2079  
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DB 2080 ctatgacgctttgatttcatatgctcgtggtacacatatctcaacagacacaaagaagaa 2139  
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DB 2140 attttgctgggctcttcgattccacaatcaaatatgatacaggggttaagatgttgt 2199  
QY 721 gaagcagagactgacagacatgttacagaaaaagttaagaagaagaaggttaactaatgttc 780  
DB 2200 gaagcagagactgacagacatgttacagaaaaagttaagaagaagaaggttaactaatgttc 2259  
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DB 2260 ttgatgatatactgagattgtgaagtggtgagatgagacgatttccaactgaa 2319  
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DB 2320 gacaatgcagggagctgaactactgttgaactaccgtaagtatgaagctgttatgct 2379  
QY 901 ggtgtgaagaattttcttcttgagagacttcaatgaactaagaatagaagttgaactc 960  
DB 2380 ggtgtgaagaattttcttcttgagagacttcaatgaactaagaatagaagttgaactc 2439  
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DB 2500 caaatcgagatgaatgtcaacggttaccacactaatatgtcgtgttcagagagctcttc 2559  
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DB 2560 aaatcctaaagagacataagatgtgaaactgttgcctaaagatgtcaagtcactcgtc 2619  
QY 1141 acaaatgatccctgatatgaacgatttcaacgtgtgtcgttgggttgaatcagatcgaca 1200  
DB 2620 acaaatgatccctgatatgaacgatttcaacgtgtgtcgttgggttgaatcagatcgaca 2679  
QY 1201 agcgcataaaaacatagtctcttcgcattccgaaattttccagaagaacagttgatcca 1260  
DB 2680 agcgcataaaaacatagtctcttcgcattccgaaattttccagaagaacagttgatcca 2739  
QY 1261 gtgaagaatttgaatgagatcatgagctgagcgaagggttccctgaagtgtgaaaatgatgt 1320  
DB 2740 gtgaagaatttgaatgagatcatgagctgagcgaagggttccctgaagtgtgaaaatgatgt 2799  
QY 1321 gaagcagaggttgcagaagtgttgcagaagctgttcgatagatgtctagtcctcgtcagc 1380  
DB 2800 gaagcagaggttgcagaagtgttgcagaagctgttcgatagatgtctagtcctcgtcagc 2859  
QY 1381 aagaagaatctcgagatgtgaacaaaataatgaatctgtgaagtcttaatatgaatctgaac 1440  
DB 2860 aagaagaatctcgagatgtgaacaaaataatgaatctgtgaagtcttaatatgaatctgaac 2919  
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DB 2980 gtatcatccagaatgttcatatctctgtatgtataaataatgcagcccttaagcgtgtg 3039  
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DB 3040 actggtgataaatttaattatgttccctatggtcttataaggcctctcttaacccgtga 3099  
QY 1621 aatcgctcagtttgagacatctgacaacaacaacacttttgaagaagaaacccatctgtttc 1680  
DB 3100 aatcgctcagtttgagacatctgacaacaacaacacttttgaagaagaaacccatctgtttc 3159  
QY 1681 tcttttcaatcttgagccttataatgttctccaatcagaaggtgttcaattccaatta 1740  
DB 3160 tcttttcaatcttgagccttataatgttctccaatcagaaggtgttcaattccaatta 3219  
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DB 3220 ctcaaaagctcttgagccttgagacacagacagatgtggtttccctcgaagataactaagc 3279  
QY 1801 ctcatctggttgcagatccatcatgttgcagctatgcagtaatttcgatactccagaa 1860  
DB 3280 ctcatctggttgcagatccatcatgttgcagctatgcagtaatttcgatactccagaa 3339  
QY 1861 atttgcaggttgcagatccatcatgttgcagctatgcagtaatttcgatactccagaa 1920

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Db 3340 atttcaggtatggaatctgcagacatcattgttcaacggttttcgatcagataaata 3399
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    |||||
Db 3400 attttgcggaagaaatttggaaactaatgcaatgaagcatttaactgcccagattt 3459
Oy 1981 tatttcagatctgcagacatctgttcgaaaggaagcatttgcattttcaaac 2040
    |||||
Db 3460 tatttcagatctgcagacatctgttcgaaaggaagcatttgcattttcaaac 3519
Oy 2041 ttcaactatttcttacttctgtccacgttgttcgacgaaggaagtattatgggatt 2100
    |||||
Db 3520 ttacaaactatttcttacttctgtccacgttgttcgacgaaggaagtattatgggatt 3579
Oy 2101 cagaatgtcaaaaatttggaaactgagaaataaggaatgataaaaattttgggac 2160
    |||||
Db 3580 cagaatgtcaaaaatttggaaactgagaaataaggaatgataaaaattttgggac 3639
Oy 2161 tctgggctcccaaatctgtctatctatctgcagcaacttgaataattgattctatct 2220
    |||||
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    |||||
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Db 3880 ccaattgtatggagtttaactgcgatgaaagctttgtcctaataatataagttttctcaag 3939
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Oy 2581 ttaagagagtgctccctccaaacttgggaaatctgtgcacgaattcaagaagaacaaaga 2640
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Oy 2641 gacctcgaagaacacccgtgtgatgttcgtatctcaatccatgtgaagaga 2692
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RESULT 6  
AAZ50262  
ID AAZ50262 standard; DNA; 2739 BP.

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XX AC AAZ50262;
XX XX 18-MAY-2000 (first entry)
XX DE Coding region of potato Gpa2 resistance gene.
XX KW Resistance gene; Gpa2; potato; phytopathogenic nematode; chromosome 12p;
XX KW marker; IPM4c; 11IR; Potato Cyst Nematode; PCN; Globodera; nematode;
XX OS Solanum tuberosum.
XX FT Key Location/Qualifiers
    CDS 1..2739

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FT FT /*tag= a /product= "Potato Gpa2 polypeptide"
FT FT /function= "Confers resistance to phytopathogenic
FT FT nematodes of the Globodera genus"
PN WO200006754-A2.
XX PD 10-FEB-2000.
XX PR 30-JUL-1999; 99WO-NL00491.
XX PR 31-JUL-1998; 98WO-NL00445.
XX PA (CPRO-) CPRO-DLO CENT PLANTENVEREDELINGS REPRO.
XX PA (UWVA-) LANDBOUMUNIVERSITEIT WAGENINGEN.
PI Van Der Vossen EAG, Van Der Voort JNAMR, Lankhorst RMK, Bakker J;
PI Stiekema WJ;
XX DR WPI; 2000-183132/16.
XX DR P-PSDB; AAY44818.
XX PT New isolated Gpa2 nematode resistance gene from potato, useful for
PT producing plants which are resistant to nematodes and polypeptides for
PT use in nematode compositions
XX PS Claim 62; Fig 3a; 96pp; English.
CC The present DNA sequence is the coding region of the potato resistance
CC gene Gpa2, that confers resistance to infection by phytopathogenic
CC nematode of the Globodera genus. It is mapped to short arm of chromosome
CC 12 (12p), between the markers IPM4c and 11IR. This locus is associated
CC with resistance to Potato Cyst Nematodes (PCN) like G. pallida and
CC G. rostochiensis, that invade and damage the roots of Solanaceae. It has
CC nematocidal activity. A recombinant DNA sequence comprising the Gpa2
CC gene sequence can be transformed or transfected into plants, to provide
CC increased resistance to nematodes. The polypeptides can also be used in
CC nematocidal compositions and for detection and diagnosis of nematode
CC infections.
SO Sequence 2739 BP; 814 A; 498 C; 600 G; 827 T; 0 other:

Query Match 10.0%; Score 272.8; DB 21; Length 2739;
Best Local Similarity 54.7%; Pred. No. 6.5e-63;
Matches 738; Conservative 0; Mismatches 567; Indels 45; Gaps 8;

Oy 140 ttgtcaagaacttggaaaaaacaatgttttgggaaatgacgagatttgaagtagag 199
    |||
Db 113 tggagaatactcgtcaataataatggcgatcatgaggggttaacaaacttggaggttgaa 172
Oy 200 taaaggaagttgacagtgctgtgatacacaaactcaactgagactaaacagaaactgtac 259
    |||
Db 173 tcatagaggttagcatcacacaagaagaatagtgtgactcggaaatcaagaatgttttt 232
Oy 260 tggagaataataaagccagaanaaaagcgctggaaggttgcgtcaaaagcctgcac 319
    |||
Db 233 tagcaggaatbtggggaagaagaagcagagctatgtggggagtttttctgccttgac 292
Oy 320 aagtcagcagagacatgtgatcatatcttgaaagatgcgaagaagtcacaagtaagaa 379
    |||
Db 293 aagcactagaatgcatgtatccaccgtgaaacagatgtagtgcacatgcagacatga 352
Oy 380 aacaagtatcaagaagatcatgtgttcatagttttcaagtcaacaacagatatgtga 439
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Db 353 aagatctaaacacacaactagctcactctgtcagtttccctggaac--atgagtgtgac 409
Oy 440 aggttaagaacaatatgttggacgttgatgaacaaaggaacagttgttgaagaatctga 499
    |||
Db 410 agcccgagaataataatgttgccgttgaaatgaatttgagatgtgctgcgtacacttg 469
Oy 500 ctagaagctactctgggaaacccaagatcccgatgtgcggatggagtgagatagta 559
    |||||

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Db 470 ctgagag---agggaagggaactagaaagtgtctcaatcgtlaaggaatggaagcatcggga 526
QY 560 aaaaacaccttagcaaaaagatttacaatgatacatcatctatgctgttgaatgc 619
XX 527 aaaaacaccttgcgaaaaacaccttaagatgatacttaactatgtctgatttgatctc 586
Db 620 atgcttggtctacatcatcacaagcacaacaaaagaaatttgcctggtccttcgc 679
QY 587 gtgcaaaagcaactgttcaacaagatattgtgtggaatgaatgactccctaggtcctt 646
XX 680 attcccaatcaaaaatggtatgagaaggttaagttgtgtggaagagagctagcagaca 739
Db 647 ctttgacaagtgatgaaccgtatctc-----agctagcgagcc 665
QY 740 tgttacagaagaatttaagaagaagagtaactaaattgtctgtgaatgatatctgagtt 799
XX 686 aactgtcaaaaagcactcgaagaagcagagatacttgtagtcatgtgatgacataatgag 745
Db 800 gtgaagtggtggaatgctgagaagatgcttcccaactgaagaacatgacggagtcgaa 859
XX 746 cagaagcttggaatgatatataactatgttccca---gactgcgataatggaagcagaa 802
QY 860 tactgttgatctaccgtaagatgaagtaagctgttatgctgtgtgtagagaatttctt 919
XX 803 tactcctgactactcggaaatggtgaagtggtcgaataatgctgaagtaagcctctc 862
Db 920 tgcgataagcttcaatgataatgataagatgagttgagttcttcaaaagtgcagattt 979
QY 863 atacaatgcgcctcatgaatttgcgaagaattggaatttactacaacaaaagcttctg 922
XX 980 caagtgaag---cattacataatgagttcgaagctgttgaagaagcaaatgcagatgaat 1036
Db 923 aaaaagaagttcttactccctgaatttgaataatltgaaacaaatcgaattcaaat 982
QY 1037 gtacaggttaccacactactgttgcgtgtggaaggtctc---caaatctaaagga 1093
XX 983 gtggaaggttactctctgcaactacttctgtctgtcgtcctctcccaaaatcgtataa 1042
Db 1094 caataagaatgtggaacactgttgcataagaatgataatcgtacaaatgatactctg 1153
XX 1043 catgtgagtggtgcaaaatggttcggaagaatgatactggtgtaagcacaagatcttg 1102
QY 1154 atgaacagtcttcaagtgctgtgtgtgtggtgtaagtaactgttcaagaagcagataaaa 1213
XX 1103 aagcaaaatgcatgagagtgltgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1162
Db 1214 catgtcttgcgcatcttgcgaatttccagaagaacagtgatataatccagtgaagaatttga 1273
XX 1163 cgtgttctcgtatcttgcgaatttccagaagaacagtgatataatccagtgaagaatttga 1222
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XX 1223 ttgagttatggtgcgtagagaggttcttgaatgaagaagaggaagcaataagaaggg 1282
Db 1328 aggttgaagaagtgttgcgaagaagttgtcgatagatgtctgactcgtgcgaagagaa 1387
XX 1283 tggcagaagaactgtataaactgtgaagatgaagaagcttaattcttaacaaatgtga 1342
QY 1388 gtgcagatggaacaaaatgtgacatgtaaggttgcataatataatagacctgtgcg 1447
XX 1343 gtttgcgtggtggaacacagag---atgtggaatgcatgagtgcgacctgtactgtt 1399
Db 1448 tgaagagaagtccaagggagacaatttcta 1477
XX 1400 tgaaggaagctcgaacaacatgtaatttgtga 1429

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RESULT 7
AAZ50652
ID AAZ50652 standard; DNA; 2817 BP.
XX
AC AAZ50652;
XX

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DT 23-MAY-2000 (first entry)
XX
DE Coding region of potato Gpa2 resistance gene.
XX
KW Resistance; Gpa2; potato; phytopathogenic nematode; chromosome 12p;
XX marker; IPM4c; 11R; potato Cyst Nematode; PCN; Globodera; nematode;
XX nematode resistance; detection; diagnosis; transgenic plant; ds.
XX Solanum tuberosum.
XX
XX Key Location/Qualifiers
XX CDS 1..2817
XX FT /*tag= a
XX FT /product= "potato Gpa2 polypeptide"
XX FT /function= "Confers resistance to phytopathogenic
XX nematodes of the Globodera genus"
XX
XX MO200006753-A1.
XX
XX 10-FEB-2000.
XX
XX 31-JUL-1998; 98MO-NL00445.
XX
XX 31-JUL-1998; 98MO-NL00445.
XX
XX (CPRO-) CPRO-DIO CENT PLANTENVEREDELINGS REPROD.
XX (OTMA-) LANDBOUMUNIVERSITEIT WAGENINGEN.
XX
XX Van Der Vossen EAG, Van Der Voort JNMR, Lankhorst RMK, Bakker J;
XX Stiekema WJ;
XX
XX WPI: 2000-195310/17.
XX
XX P-PSDB; AAZY5004.
XX
XX Recombinant Gpa2 polynucleotide from potato, Solanum tuberosum, useful
XX to confer resistance to phytopathic nematodes of the genus Globodera in
XX transgenic plants, e.g. resistance to potato cyst nematodes in potatoes
XX
XX Claim 1; Fig 3a; 96pp; English.
XX
XX The present DNA sequence is the coding region of the potato resistance
XX gene Gpa2, that confers resistance to infection by phytopathogenic
XX nematode of the Globodera genus. It is mapped to short arm of chromosome
XX 12 (12p), between the markers IPM4c and 11R. This locus is associated
XX with resistance to potato Cyst Nematodes (PCN) like G. pallida and
XX G. rostochiensis, that invade and damage the roots of Solanaceae. It has
XX nematocidal activity. Recombinant DNA sequence comprising the Gpa2
XX gene can be used to produce transgenic plants with increased resistance to
XX nematodes. The polypeptides can also be used in nematocidal compositions
XX and for detection and diagnosis of nematode infections.
XX
XX Sequence 2817 BP; 846 A; 503 C; 626 G; 842 T; 0 other;
XX
XX
XX Query Match 10.0%; Score 272.8; DB 21; Length 2817;
XX Best Local Similarity 54.7%; Pred. No. 6.5e-63;
XX Matches 738; Conservative 0; Mismatches 567; Indels 45; Gaps 8;
XX
XX 140 ttgtcagaacttggagaacaaatgttttggggaaatgacgatttgaagaggg 199
XX 113 tggagaatctccgcaataataatggtcgaatcagaggggtttaaactcttggagattgaa 172
Db 200 taaggaagttgcgaagtgtcgtgatacacaaatcgaactgagatacagaagaatgttac 259
XX 173 tcatagaggtagatacacacaacagaagatattgttgcactcggaaatcaagaatgttttt 232
QY 260 tggagaataataaagccagaacaaaagcgctcgaaggttctgcataagcctcgcaac 319
XX 233 tagcacggaatgtggggaaaagacagcgctatgtgggggaatttttctgccttggaaac 292
Db 320 aagtgcagagagcatgatactatctgtgaagagtcgcaagaatccaagataagaa 379
XX

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Db 293 aagcactagaatgcatgtatccaccgtgaaacagtgatgagcaacatcggaacatga 352  
 Qy 380 aacaagatcaagaagatcatgttgcatttccaggttcaacaacgatatttga 439  
 Db 353 aagatctaaacacaaactagctactgtcagtttaccctgaac--atgagtgtgagc 409  
 Qy 440 aggttaagaacaatagtgtgagcgtgagatcaagaagaacagttgttagaagatcga 499  
 Db 410 agccgagaataatagtgtgagcgtgaaatgaatttgatgagtcgagcgaacttg 469  
 Qy 500 ctgaaagctactctgaggaacccaagatcccgatttcggatgagggacatagta 559  
 Db 470 ctgagaag--aggaagggactagaaagtgtctcaactgtagagatggagacatcgga 526  
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 Db 527 aacaacattgtgctgaacactctatagatccttactctatgtctcgtattgatac 586  
 Qy 620 atgctcggtctacatatactcaacagacacaaaaggaatttgcctggcctctgc 679  
 Db 587 gtgcaaaagcaactgttccacaagatgtgtgagaatgttactcctgagcctctt 646  
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 Db 647 cttgacaagtgtgacactgtatc-----agctacgcgagc 685  
 Qy 740 tgttacagaagaagtttaagaagaaggttactaattgtcttgatgatatctgagtt 799  
 Db 686 aactgcaaaagcaactgaaagcagagatctgtgacttgatctgattgacatagta 745  
 Qy 800 gtgaaagtgtgagatgctgagagacagcttccaaactgaaagacatgcaggagtcga 859  
 Db 746 cagaagcttggagatgataaaacatgtttccca--gactgcgatatgaaacagaa 802  
 Qy 860 tacttctgactaccgtaatgtagaagtagctgtgtagtgcgtgtgtagaagatttctt 919  
 Db 803 tactcctgactactcgtgaatgtagaagtgctgataatgtagcagctcagctcctc 862  
 Qy 920 tggagatgagctcattgatacaagaatgagagttgagctcttccaaaagtgcagattt 979  
 Db 863 atcacatgcgctcctatgtaatttgcaaaagttggaatttactaacaaaaagatctt 922  
 Qy 980 caagtgaaag--cattaccatagtgctcgagcagctgtggaagaagaatcgcaatga 1036  
 Db 922 aaaaagaaggtcttattcctccgtaatttgaaatatgggaaacaatgcatlaaat 982  
 Qy 1037 gtcaaggttaccactaattgtcgtgtgtagcagggctct--caactctaaagga 1093  
 Db 983 gtgaggggttacccttagcaatttactgtgctgagcctctcccaaatcgttaaa 1042  
 Qy 1094 caatagaagattggaacactgttgcataaagatgcaagatcgtctcaaaatgactctg 1153  
 Db 1043 catgtagaagatggaacactgttgcggaatgtagctgtgtagtagcagacagactctg 1102  
 Qy 1154 atgaacgagtgtcagctgtgtgtgtgtagttagcagctacttgaacgagatataaa 1213  
 Db 1103 aagaacaatgcatgagagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1162  
 Qy 1214 catgtctgtcatcttgcgaatttcccaagaagacagtgatattccagtgaaagattga 1273  
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 Db 1223 ttgagttatggccgttgaaggggttcttgaatgaagaaggggaaagaatgagaag 1282  
 Qy 1328 aggttgaagaagttgttgaagaagctgtgtagatgtctagcctcgttagaagaagaa 1387  
 Db 1283 tggcagaagaactgtatataacgaactgtgtagatgaagatcctaattctacacaatgtga 1342  
 Qy 1388 gtgcagaatggaacaacaatgatcatgtagaagttcagttcgaataatagactgtgag 1447  
 Db 1343 gtttctgtggtggaacacagag--atgtggaatgcatgtgtgacccgtgacactctgtt 1399

Qy 1448 tgaagaagttcaagaaggagacatttga 1477  
 Db 1400 tgaaggaaagctcgaacacatgatttga 1429  
 RESULT 8  
 ID AAS03713 standard; cDNA; 3683 BP.  
 XX AAS03713;  
 XX 29-AUG-2001 (first entry)  
 XX  
 DE DNA encoding Rx 25, a modified resistance protein.  
 XX  
 KW Rx: modified resistance; NBS; LRR; cell death; autoactivator;  
 KW nucleotide binding site; leucine rich repeat; pathogen resistance;  
 KW plant; ss.  
 XX  
 OS Solanum tuberosum.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 37..2850  
 FT /\*tag= a  
 FT /product= "Modified resistance protein 25"  
 XX  
 PN W0200129239-A2.  
 XX  
 PD 26-APR-2001.  
 XX  
 PE 12-OCT-2000; 2000MO-GB03930.  
 XX  
 PR 15-OCT-1999; 99GB-0024483.  
 XX  
 PA (PLAN-) PLANT BIOSCIENCE LTD.  
 XX  
 PI Bendahmane A, Baulcombe DC;  
 XX  
 DR WPI: 2001-290924/30.  
 DR P-PADB; AA002143.  
 XX  
 PT Modifying activation characteristics of plant resistance proteins to  
 PT produce autoactivator polypeptide capable of activation in absence of  
 PT elicitor, by introducing modifications in amino acid sequence of  
 PT protein -  
 XX  
 PS Disclosure; Page 46-60; 77pp; English.  
 XX  
 CC The sequence represents the coding sequence of Rx clone 25, a modified  
 CC resistance autoactivator. Rx encodes an NBS-LRR polypeptide having a  
 CC nucleotide binding site (NBS), leucine rich repeat (LRR), and which  
 CC mediates cellular response leading to pathogen resistance and/or cell  
 CC death or dysfunction in response to an elicitor. The Rx was modified by  
 CC introducing modification to the amino acid sequence to produce an  
 CC autoactivator polypeptide, capable of activation in absence of an  
 CC elicitor. Decoupling of resistance response from its natural elicitor is  
 CC useful for developing novel pathogen resistant plants. The modified  
 CC resistance proteins are useful for conferring resistance to non-natural  
 CC agents or stimuli and also for investigating resistance response pathways  
 CC and protein interactions e.g. with activators and repressors.  
 XX  
 SO Sequence 3683 BP; 1149 A; 635 C; 782 G; 1117 T; 0 other;  
 Query Match 10.0%; Score 272.8; DB 22; Length 3683;  
 Best Local Similarity 54.7%; Pred. No. 7.4e-63;  
 Matches 738; Conservative 0; Mismatches 567; Indels 45; Gaps 8;  
 Qy 140 tgcagaagacttgaagaacaatgttctggggaatgacggatttgaagtagagg 199  
 Db 149 tggagaatccctgcataataatggtgagcatgaggggttaacaacttggaaagttagaa 208

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QY 200 taagaagattgcaagtgctgctgaatacacaattcaactgagactgacagtac 259
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 209 tclgtgaagtagcatatacacaacagaagatacgltgactcggaatcaagaattgttlt 268
QY 260 tgggaagaataaagccgcaaaaaaagcgctgcgaaggttctgcgaagcctgcaac 319
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 269 tagcacagatttggaggaagaagacagagctatgtggagatlttcttcgttcggaac 328
QY 320 aagtgacagagacatgcatatctggaagagtcgacaagaatccaagataaaggaa 379
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 329 aagcactaagatgcatgtgttccaccgtgaacaagtgatgccaatcggaacagtga 388
QY 380 aacaagatcaagaagatcatctggttcatgatttttccaagttcaacaacgataatttga 439
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 389 aagatctaaacacacaactagctgcgtgtcagttactctg--aactlgtgtgagc 445
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Db 446 agcccgagagataataatggttgcctgtgaataatgtaatttgatgtagtgcgtgatacactg 505
QY 500 ctgaagctactctggygaacccaagatcccgatctgcggaatggyagagatagta 559
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Db 506 ctgagag--aggaagggagactagaaggtgtctcaatcgtaggagatggyagcgcgga 562
QY 560 aacaacacctagcaaaagaagtttaacatgataatcaatctctatgcccgttttgatgttc 619
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Db 563 aacaacacttgcatacaaaactctatagtcacgacacaaagaataatttgcgcgggccttcgc 622
QY 620 agcgctggctaccatcatctcaacgacacaaagaataatttgcgcgggccttcgc 679
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QY 680 attccaacatcaaaatgtagtacaaggttaagatgattggtgaagcagagctagcagaca 739
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Db 683 cttgacaagtagtgaactgat-----gactagctagcggacc 721
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Db 722 gactcgaanaagcaltcgaagagcgagabactgtgtagtcattgtagacataatgtagca 781
QY 800 ggaaggtgtgagatgcygtagagacgagcttcccaactgaagaacatgagggagcagaa 859
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Db 782 cagaagccttggagatataataaactatgttccacagacgtataat---ggaagcagaa 838
QY 860 tactgttgaactaccgtaatgtagtaagtagctgtttagtgcgtgtagagaatttctt 919
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Db 839 tactcctgactactcgaatgtggaagtgtgcaatatactgttcaagtaagccctc 898
QY 920 tgcgagtagagcttcatgtagtaagatgtagtcttcttccaagaatgtagcaattt 979
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Db 899 atcacactgacctcagaaattttagacgaagttggaatttactaacaacaaagatcttgc 958
QY 980 caagtgaaag---cattacataatgattcgaagactgttggaaagcaaatcgacagat 1036
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Db 959 aaaaagaagagttcttacttctcctgaatttgaataatattggaaacaacatgcaat 1018
QY 1037 gtcaaggggttaccactaactattgtcgtgtgagcaggtctct---caacttaaaagga 1093
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1019 gtgagagattactacttaagataactgtgtgtggaactctctccaatgtgcaaa 1078
QY 1094 caatagaagattggaanaagctgtgctaagaatgtaacgcatcgtcacaaatgtagccg 1153
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Db 1079 gatttgatgtagtggcacaagaatgtgggaaatgtaagttcgtgcgtttagcacagatcccg 1138
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Db 1139 aagcaacatgcatgtagagaggtgtgctgtgagtagcatcactgtcttccaccctaaac 1198
QY 1214 cgtgcttctgcatcttgcgaatttttccagaagacagtgatattccagtggaagaatttga 1273
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Db 1199 cgtgttcttctgatttgcgaatttccacagagataaacaagatttctgtaaatgtaactgt 1258

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QY 1274 tgaatcatgtagtgcgtaggggttctctga-----agttgaaatgatttgaagag 1327
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Db 1259 ttgagtagtggcctgtgagggagattttagaataaagaagggaaaaagatagaagag 1318
QY 1328 aggttgaagaagtglttgcagaagcctgtgcagatgtagtgccttcgtcagaagaagaa 1387
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Db 1319 tggcacacaatgataaacaagactatagatagaagacttaatttcaatccacaattt 1378
QY 1388 gtccgaatggaaacaaaatagatcatgtaagttcatgattcacaatataagactgtgc 1447
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Db 1379 gtttcgttggaacaataagaag---ctgtggaatgtagatgtgacccgtgaactcgt 1435
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RESULT 9
AAZ50264
ID AAZ50264 standard; DNA; 10329 BP.
XX
AC AAZ50264;
XX
DT 18-MAY-2000 (first entry)
XX
DE Genomic DNA of potato Gpa2 resistance gene.
XX
KW Resistance gene; Gpa2; potato; phytopathogenic nematode; chromosome 12p;
KW marker; IPM4C; 11LR; Potato Cyst Nematode; PCN; Globodera; nematode;
KW nematode resistance; detection; diagnosis; transgenic plant; ds.
XX
OS Solanum tuberosum.
XX
FH Key Location/Qualifiers
FT misc_signal 1..4874
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FT FT /note= "Gpa2 regulatory region"
FT CDS 4875..7850
FT FT /*tag= b
FT FT /product= "Potato Gpa2 resistance protein"
FT FT /note= "This region is specifically claimed"
FT exon 4875..7585
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FT FT /number= 1
FT intron 7586..7822
FT FT /*tag= d
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FT FT /note= "Located within the coding region of Gpa2 gene"
FT exon 7823..7850
FT FT /*tag= e
FT FT /number= 2
FT FT /note= "Includes the stop codon, TGA"
FT intron 7942..8053
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XX
PN WO200006754-A2.
XX
PD 10-FEB-2000.
XX
PF 30-JUL-1999; 99WO-NL00491.
XX
PR 31-JUL-1998; 98WO-NL00445.
XX
PA (CPRO-) CPRO-DLO CENT PLANTENVEREDELINGS REPROD.
PA (UYMA-) LANDBODUWUNIVERSITEIT WAGENINGEN.
XX
PI Van Der Vossen ENG, Van Der Voort JNMR, Lankhorst RMK, Bakker J;
PI Stiekema WJ;
XX
DR WPI; 2000-183132/16.
DR P-PSDB; AAY4818.

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FT      /note= "This region is claimed (Claim 13)"
XX      WO200006753-A1.
XX      10-FEB-2000.
XX      31-JUL-1998; 98WO-NL00445.
XX      31-JUL-1998; 98WO-NL00445.
XX      31-JUL-1998; 98WO-NL00445.
XX      (CPRO-) CPRO-DLO CENT PLANTENVERDELINGS REPROD.
XX      (UYWA-) LANDBOUDUNIVERSITEIT WAGENINGEN.
XX      Van Der Voosen EAG, Van Der Voort JNMR, Lankhorst RMK, Bakker J;
XX      Stiekema WJ;
XX      WPI: 2000-195310/17.
XX      P-PSDB: AAY45004.
XX      Recombinant Gpa2 polynucleotide from potato, Solanum tuberosum, useful
XX      to confer resistance to phytopathic nematodes of the genus Globodera in
XX      transgenic plants, e.g. resistance to potato cyst nematodes in potatoes
XX      -
XX      Claim 21; Fig 3c; 96pp; English.
XX      The present sequence is the genomic DNA encoding potato Gpa2 resistance
XX      protein. It is inserted in the pBINRGHZ plasmid which is used to
XX      transform host plant cells to produce transgenic plants. Gpa2 confers
XX      resistance to infection by phytopathogenic nematode of the
XX      Globodera genus. It is mapped to short arm of chromosome 12 (12p),
XX      between the markers IPM4c and 111R. This locus is associated
XX      with resistance to potato Cyst Nematodes (PCN) like G. pallida and
XX      G. rostochiensis, that invade and damage the roots of Solanaceae. It has
XX      nematocidal activity. Recombinant DNA sequence comprising the Gpa2
XX      gene can used to produce transgenic plants with increased resistance to
XX      nematodes. The polypeptides can also be used in nematocidal compositions
XX      and for detection and diagnosis of nematode infections.
XX      Sequence 10329 BP; 3150 A; 1542 C; 1924 G; 3713 T; 0 other;
SQ
Query Match 10.0%; Score 272.8; DB 21; Length 10329;
Best Local Similarity 54.7%; Pred. No. 1.2e-62;
Matches 738; Conservative 0; Mismatches 567; Indels 45; Gaps 8;
QY      140 tgcctaagaacttggaaaacaatgttttggggaaatgacgcgatttttgaagtagag 199
DB      4987 tggagaatacctgcgaataaataatggcgatcagtagagggttaacaactcttggaaattgaa 5046
QY      200 taagaagaattgcaagtgtctgtaatacacaaatccaactgagactaagaactgtac 259
DB      5047 tcatagaggttagcatacacacagaagatattgttgactcggaatccaagaattgttttt 5106
QY      260 tgggagaataataaagccagaaaaaagcgctgcgaaggttgcgtaaacctgtcaac 319
DB      5107 tagcaggaatgttggggaagaagcagggcctatgttggggatttttctgccttggaac 5166
QY      320 aagtcagcagagacatgatatctatctggaagagtcgacaagaatccaagtaagaa 379
DB      5167 aagcactagaatgcatgtattccaccgtgaaacagtgatggcaacatcgacagcatga 5226

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QY      440 aggttaagaacaatatgtttggacgtgatgataaagaagaaagttttgaagatga 499
DB      5284 agcccgagaataataatggttgcgcgtgaaaatgaatttgagatgacgtgacaaactg 5343
QY      500 ctagaactactctggygaaccacaagttcacccgatctgcggatgtggagacatagta 559
DB      5344 ctagagg---aggaaagggaactagaagttgtctccaatcgttagggatggagcctggga 5400
QY      560 aaacaaccttagcgaaaaaagatttacaaatgataatcaattcctacgttttgatgc 619
DB      5401 aaacaacttggctgcgaaaaactctatagttgctccattacattatgtctcgaattgatattc 5460
QY      620 atgcctgggtacacatactcaacagacaacaaaaggaattttgcttggtccttcgc 679
DB      5461 gtgcgaagaagcaactgtttccacaagagatattgttgagaatgtaactcctgagcctcttc 5520
QY      680 attccacaatcaaaatgagatgacaggggttaagatgaltggtgaagcagagctagcagaca 739
DB      5521 cttagcaagtgatgacacctgattac-----agctagcggacc 5559
QY      740 tgttacagaanaatttaagaagagaagagctactaatgtgtcttgatgatatctggagt 799
DB      5560 aactgcgaagaagcatctggaagcagagatcattgtgtagctatgatacatatgagacta 5619
QY      800 gtgaagtgtggatggtgcgttagacgagttcttccaactgagaacatgcaggagtcgaa 859
DB      5620 cagaagcttgggtatgataaaactatgttccca---gactcgataataggaagcagaa 5676
QY      860 tactgttgactaccgtaatgataatgaaagctgtgtatgctgtgtgtagagaattttct 919
DB      5677 tactcctgactactcggaaatgtggaagtgtgtaataatgactagctcaggaagcctctc 5736
QY      920 tgggagtgagctgacatgagatgagatgagaggttggtcttttcaaaagtcgacattt 979
DB      5737 atcacatgcgcctccatgaaatttggacgaagtttggaaatttactacacaaaagatcttt 5796
QY      980 caagttaag---cattacaatgaatgcagactgtgcagactgttggaaaagcaatgcagatgaat 1036
DB      5797 aaaaagaagttcttattctcccgaaatttgaataatttgggaacaaatgcatgaaat 5856
QY      1037 gtcaaggttaccactaactattgtcgtgtgacaggctctc---caacttaaaagga 1093
DB      5857 gtggaaggttaccctcagcaatattactgtattgtcgtgactctctccaaatcagtaaaa 5916
QY      1094 caatgaagaattggaaaactgttgcctaagaatgtaagatgcatctgcacaaatgactcgt 1153
DB      5917 catltgattgagtggaataatgttgcggagaatgtaatgcttcgtgtgtaagcagacatcttg 5976
QY      1154 atgaacgatgttcaacgtgtgcttgggttgaatgatacactgtgacaacgcatactaaaa 1213
DB      5977 aagcaaaatgcatgagagagtggtgcttgaatttgaatccactgctcttcaccctaaac 6036
QY      1214 catgtcttctgcatttcggaattttccagaagacagtgatatactcagtggaagaatttga 1273
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QY      1328 aggttgagaagtgttgcagaagctgtgcataagatgtctagtcctcgtcagcaagaagaa 1387
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QY      1388 gtccagatgtgaacaaaataatagatcatctgaagtttcatatgataatataatgtgtgg 1447
DB      6217 gtttcatgtgggaacaacacagag---atgtggaatgcatatgtgacccgtgaactctgtt 6273

```





OY	1037	gtcaaggggttaaccataactctgtcgtgtgtgtcagaggtcctc---caatctaaagga	1093
Db	3231	gtgagagatctaccttaagcaattactctgtgattgtctgtgactctctctccaaatggttcaaa	3290
OY	1094	caatagaagattggaaaactctgtgtcaagatgtcgaagtcattcgtccaaatgtctctg	1153
Db	3291	gattcagaagatgtgaaaagaatttggggaaaatgttaagtctgtctgttcagacagatccttg	3350
OY	1154	atgaacgaatgttcaacgtgtgtcttgggtttgaagttacgatacctttgacaagcgtatcaaaa	1213
Db	3351	aagccaatgacatgagagatgtgtgtctttgagttacatccatcattgtctctccctcaaaac	3410
OY	1214	catgtctctgtatcttggaaattttccgaagaacagtgatattccagtyaagaatttga	1273
Db	3411	cggtttctctgatttttgaatttccacagagatgaaacagatttctgttaattgtacttg	3470
OY	1274	tgaagatcatgtacgtgcagaggggtctcga-----agttgaaaatgtattggaaagag	1327
Db	3471	ttgagttatgtgccttgaaggagattttttgaagaagaagggaaaagacatagaagag	3530
OY	1328	aggttgagaagatgtttgcagaagagctgttcgatatagtctagtctcgtccagcaagaga	1387
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OY	1388	gtcgaagatgaacaaaaattatacatgtaaagtttcatgatcctaataatbtgacctgtgcg	1447
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OY	1448	tgaagaaattcaaaagggagaacatttta---tcctgaagaacattgtcttgcagttat	1504
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OY	1505	catatccagaatgtttcatactctctgtatgtatataaaatgaagccctttaagcgcgtgactg	1564
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OY	1565	gtgaatgaatttaattattgtctcctatgtgtcttatatagggctctcttta-----	1612
Db	3768	tggaaagaatgtgcttgtgtgtcgtaaagtgaggtcattcatatcatcatatgtgtgtgat	3827
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Db	3828	tgaatgcgcacaacacgaaattgtcttccaagctagtgaagagctactagactctgtttga	3887
OY	1661	aacgaaccaattcgttttctctttccaactctgaagccttatatatgttctcaaatcag	1720
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OY	1772	ttgatgtttccctcgagagataactaagcctcatctgtgtg-----agttacc	1819
Db	4008	taatagacatttccctctaactgataccaagcctatctctatctgtcaaacattttaaactaac	4067
OY	1820	tatcatgttccagctatgggaatttgaatgtacctccgaagaatttgaagttatgagatc	1879
Db	4068	ttccatttcccaattatcatccttcataattaccatcogaaaatttgaagatgcacaact	4127
OY	1880	tgcagacatcatatgttccaacggtttcgatcagataataaatttttgcgtgaagaaatt	1939
Db	4128	tgaagaaagcgtgtgatgtggtgcgtgaattacttgcgtgagatcatgagcttacaagaaagat	4187
OY	1940	gggaactaatgcaatt---aagcactttaaactgcccagattttatttggcagaattgccc	1996
Db	4188	tgtgtttgaaaatttgcgaatgcctcaatcaatgaaacctcgttatgtacagaggtct	4247
OY	1997	caagtgtatcgtttgacaagaagagacactgtgatttccaactta--caactatttct	2055
Db	4248	tttttagactatttcccaattaaagaagtgcagaatttttgggtctccagaagaacttcc	4307

Oy	2056	tactgtctccacgltgtlgtgcaggaaggatattatgggagtctcaagatgtccaanaa	2115
Db	4308	gaataagcagaacctgtatgtatttcgcacttatcatcagtcgaagtgcacattc	4367
Oy	2116	ttagaatcacagggaataaagatgactactaaagtttccggactctgtgccaac	2175
Db	4368	gtttatatcatccatgatgtctgtcttctctaanaaacctgcacttcaggtttaagc	4427
Oy	2176	aactctgtcatctgcagcaacttgaaaatattgagtcctatatctgt-----gattata	2230
Db	4428	aagatccctcgaggttctcgcagcgaataatttcacaaaagagattgatttcgggggaactg	4487
Oy	2231	gcctttgccaatgacatcttcacaatgcgaagaagcctttcccaogaacgtccaaagattga	2290
Db	4488	caactccaacttaactcttaactctccgcgagatgctttcccaaaaaccttaagaatttaa	4547
Oy	2291	agtt--ggaaagaacttatctaagctgtgcatacttgacatcatcagcttgagttgccta	2347
Db	4548	c tttagggagagatctctcgtlbgcataggaaagatttgacatcttgttgtaaattccc	4607
Oy	2348	acc tttaggtgtcgtgaagctgcatgatgacgcgttgtgtggtggaagaatggcatccaattg	2407
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Oy	2408	ttatggatttaactgcattggaagcctttgtctaattaaatagtttctcaagttctgga	2467
Db	4668	aggaaaggttccctcactgaagttcctgttctctgtgatagtatcatcgcgaactgga	4727
Oy	2468	aagccacaatgtacaatttccctgcctctgagcgccatcagatgaagattgacaaaaatt	2527
Db	4728	gaactgttagtgcataccttcgcgaaccttgaaagagattatctttaagagattgcgtaatt	4787
Oy	2528	tgaagaagatacccatgtgattctgcagatatacacacactacagcgtgattgattaaag	2587
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Oy	2588	agttgtctcccaactctggggaaatctgtgcagaaattcagaagaacgaagaagactcg	2647
Db	4848	actgtcaacaacatcgtgtgtaattccgcgaagcaaatattcaacagagacatccaagacaact	4907
Oy	2648	gaacaacacctgtlgatgtctgtatctccaatccatitgaagagagatgattcgtatcag	2707
Db	4908	atggaagctctatcgtagaggtccataactcgtcaactcttgtaagaacatcttctcgtgctt	4967
Oy	2708	aagacaatta 2717	
Db	4968	tacacaata 4977	
 RESULT_12			
ID	AAZ37154	standard; CDNA; 3066 BP.	
XX	AAZ37154;		
XX	01-FEB-2000	(first entry)	
DE	Partial nucleotide sequence of Rx gene cDNA.		
XX	Potato; Rx gene; resistance gene; potato virus X; PVX; transgenic plant;		
KW	broad spectrum extreme resistance; Narcissus mosaic virus; NMV; NVX; VMV;		
KM	Nandina virus X; Viola mosaic virus; Cymbidium mosaic virus; CYMV; Poplar		
KW	Poplar mosaic virus; White clover mosaic virus; WCLMV; activate; ss.		
XX	Solanum tuberosum.		
OS	Key	Location/Qualifiers	
FH	CDS	1..2864	
FT		/tag= a	
FT		/product= Rx	
FM		/note= "Resistance gene product"	
PN	W09954490-A2.		

XX 28-OCT-1999.  
 PD 16-APR-1999; 99MO-GB01182.  
 XX 16-APR-1998; 98GB-0008083.  
 PR (PLAN-) PLANT BIOSCIENCE LTD.  
 XX  
 PI Bendahmane A, Baulcombe DC, Kanyuka KV;  
 XX WPI; 1999-634006/54.  
 DR P-PSDB; AA52152.  
 XX  
 PT New isolated plant virus resistance gene, used to produce transgenic  
 PT plants with resistance to virus infection  
 XX  
 PS Claim 4; Page 87-90; 124pp; English.  
 CC This is the DNA sequence of the potato Rx gene. The Rx gene is a  
 CC resistance gene which confers extreme resistance against potato virus X  
 CC (PVX). Sequence AA52152 is the Rx gene including introns. The Rx gene  
 CC can be used to create a recombinant vector which encodes the Rx  
 CC resistance polypeptide AY52152, this vector can be used to transform  
 CC plant cells to produce a transgenic plant with resistance to PVX. The Rx  
 CC gene can be used to engineer resistance traits, preferably broad spectrum  
 CC extreme resistance, into plants. The Rx gene can also be activated by  
 CC non-PVX viruses, e.g. Narcissus mosaic virus (NMV), Nandina virus X  
 CC (NVX), Viola mosaic virus (VMV), Cymbidium mosaic virus (CYMV), Poplar  
 CC mosaic virus (PopMV) and white clover mosaic virus (WCLMV). Rx can be  
 CC used to offer specific protection against this group. The Rx gene  
 CC sequence can be used to create antibodies specific for Rx. The antibodies  
 CC can be used to down-regulate Rx activity and also for the detection,  
 CC identification or isolation of Rx or homologues.  
 SQ Sequence 3066 BP: 913 A; 533 C; 675 G; 945 T; 0 other.

Query Match 9.9%; Score 269.6; DB 20; Length 3066;  
 Best Local Similarity 54.5%; Pred. No. 4.9e-62;  
 Matches 736; Conservative 0; Mismatches 569; Indels 45; Gaps 8;

QY 140 ttgtcaagaacttggagaaacatgttttggggaatgacgatttgaagtagg 199  
 DB 163 tggagaaatcccgcatataaagcgagatcagaggggttaacaacttggagattgaaa 222  
 QY 200 taagaagaattgcaagtgctgtaatacacaatcaactgagactaagaagactgtac 259  
 DB 223 tctagaggtagcatacacacagaagatgtgtgactcgatcaagaatgttttt 282  
 QY 260 tggggaataataaagccagaaataaagcgctgcaaggttccgtcaaaagcctgcaac 319  
 DB 283 tagcagaatttggaggaagaaagcaggtatgtgtggagatttttctgcctggaac 342  
 QY 320 aagtagcagagacatgcatatctgtgaagagtcgaagaagatccaagaataagaa 379  
 DB 343 aagcactagaatgcatgtatccaccgctgaacagtgatgacacatcgacagcatga 402  
 QY 360 aacaagtcaaaagaaatcattgttcaatgttttcaagttcaacaacgataltttga 439  
 DB 403 aagatctaaacccaactagctcgttcagtttaacctg---aacatgtgtgagc 459  
 QY 440 aggttaagaacaatatgttggagtgatgataaagaaacagtttttagaagatctga 499  
 DB 460 agcccgaaatataatgtgttggccgtgaataatgaaatgtatgtcgtatcaactgt 519  
 QY 500 ctagaagatcttggggaacccaagtcacccgattgtctgctgagggagagcctagta 559  
 DB 520 ctagaag---aggaagggaaactagaagttgtctcaatcgttagggagtcgagga 576  
 QY 560 aaacaaccttagcaaaagagtttaacaatgataatcaatctatgacggtttgatgt 619  
 DB 577 aaacaacttggctacaaaactcatatagtgatcgtcattatgtctcgatttgaatttc 636

QY 620 atgacctggtctacacatctcacagcacaacaaagaaatttgcgtggtcttcgc 679  
 DB 637 gtgcaaaagaaactgtttccacaagagttatgttgagaaatgactccttagcctcttc 696  
 QY 680 attccacatacaaatgtatgacaggttgaagatgattgtgtgaagcagagctagcagaca 739  
 DB 697 cttgcaagaatgtatgaacctgtat-----gatacgttagcggacc 735  
 QY 740 tgttacaagaagaatgaaagagtaagagtaattgtctgttgatgatatgaggtt 799  
 DB 736 gactgcaaaagaaatctgaagagcagggagatattcgttgatcattgacatacagacta 795  
 QY 800 gtgaagttggtatggtcggtgagacgatttccaaactgaaagacatcgagggatcgaa 859  
 DB 796 cagaagcttggatgatatataaactatgttccagactgtataat---ggaagcagaa 852  
 QY 860 tactgtgactaacccgtatgataagtaagttgttctgtggtgtagaattttctc 919  
 DB 853 tactcctgactcaccctcggaatgagagctgctgaatatgtcaggttcaggttagagctctc 912  
 QY 920 tgcgagtgccttcaatgataaagatgagagttgagttctttcaaaagtcagacattt 979  
 DB 913 atcaatgctcctatgatttgaacgaaggttgaaatttaactacacaaaagatcttg 972  
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 DB 973 aaaaagaagttcttattcttctcgaatttgaataatgtggaacaaatgtactaataat 1032  
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 DB 1093 gattagaatggtgcaagaagatttggggaataatgaaattcgtcgttgaacagactcgt 1152  
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 DB 1153 aagcaacaatgacagagaggtgtgtgcttggattacacacactgtcctcctccttaaaac 1212  
 QY 1214 catgtcttcgcatlctcgaaatttccagaagaacagtgatattcagtggaagaatttga 1273  
 DB 1213 cgtgtttctgtatttctgcaatttccagagagatgaacagattctgtcaaatgaaactgt 1272  
 QY 1274 tggatcatgataatggtcgtgaggggttccctga-----agttgaaatgtattggaagag 1327  
 DB 1273 ttgaattatggtcgtgataagagatttctgaaatgaagaagaggaacacatagaagag 1332  
 QY 1328 aggttgaagagttgttgcagaagactgttcgatataatgctcgtcgtcagcaagaagaa 1387  
 DB 1333 tggcaacaacatgataaagaactatagatagaagacttaatttccacccaatttta 1392  
 QY 1388 gtccgaatggaacaaataatagatcatgcaagttcaatgataatataatgacgtgtgcg 1447  
 DB 1393 gtttctgttgaacaaatagaag---ctgtgaatgataatgattgacccgtgaactctgt 1449  
 QY 1448 tgaagaagaatcgaagggagaacatttta 1477  
 DB 1450 tgaaggaagctcgaacacatgaattttgtga 1479

RESULT 13  
 AAS03715  
 ID AAS03715 standard; cDNA; 3014 BP.  
 XX  
 AC AAS03715;  
 XX  
 DT 29-AUG-2001 (first entry)  
 XX  
 DE DNA encoding Rx 72, a modified resistance protein.  
 XX  
 KW Rx; modified resistance; NBS; LRR; cell death; autoactivator;

KW nucleotide binding site; leucine rich repeat; pathogen resistance;  
 plant; ss.  
 OS Solanum tuberosum.  
 OS Synthetic.  
 XX

Key Location/Qualifiers  
 FT 42..2855  
 FT /\*tag= a  
 FT /product= "Modified resistance protein 72"  
 XX

PN MO200129239-A2.

PD 26-APR-2001.

PF 12-OCT-2000; 2000MO-GB03930.

PR 15-OCT-1999; 99GB-0024483.

PA (PLAN-) PLANT BIOSCIENCE LTD.

PI Bendahmane A, Baulcombe DC;

DR WPI: 2001-290924/30.

DR P-PSDB: AMU02145.

PT Modifying activation characteristics of plant resistance proteins to  
 produce autoactivator polypeptide capable of activation in absence of  
 PT elicitor, by introducing modifications in amino acid sequence of  
 PT protein -  
 XX

PS Disclosure: Page 46-57; 77pp; English.

XX The sequence represents the coding sequence of Rx Clone 72, a modified  
 CC resistance autoactivator. Rx encodes an NBS-LRR polypeptide having a  
 CC nucleotide binding site (NBS), leucine rich repeat (LRR), and which  
 CC mediates cellular response leading to pathogen resistance and/or cell  
 CC death or dysfunction in response to an elicitor. The Rx was modified by  
 CC introducing modification to the amino acid sequence to produce an  
 CC autoactivator polypeptide, capable of activation in absence of an  
 CC elicitor. Decoupling of resistance response from its natural elicitor is  
 CC useful for developing novel pathogen resistant plants. The modified  
 CC resistance proteins are useful for conferring resistance to non-natural  
 CC agents or stimuli and also for investigating resistance response pathways  
 CC and protein interactions e.g. with activators and repressors.  
 CC  
 XX

SQ Sequence 3014 BP; 891 A; 555 C; 674 G; 894 T; 0 other;

Query Match 9.9%; Score 268; DB 22; Length 3014;

Best Local Similarity 54.4%; Pred. No. 1.3e-61;

Matches 735; Conservative 0; Mismatches 570; Indels 45; Gaps 8;

QY 140 ttgtcaagaacttggaaacaatgttttggggaatgacgagatttgaagtagag 199  
 DB 154 tggagaaatccctgcaatataatgtggcgatcaatgaggttaacaatcttggagttgaa 213  
 QY 200 taagaaagtgtcaagtgctgtgtaatacaaatccaactggaactaacgagacgtgtac 239  
 DB 214 tcgtlaaggtlaagcatcacacacagagatagtgtgtaactggaataaagaatgttttt 273  
 QY 260 ttggggaataataaagccagaaataaagcgctgcaaggtttcgtaacgctgcaac 319  
 DB 274 tggacaagaatttggggaagaagaagcagggctatgtgggagatttttctgctcctggaac 333  
 QY 320 aagtagcagaagacatgcatatctggaagaagtcgacaagaatccaagaataaaggaa 379  
 DB 334 aagcactagatgcatgattccacgctggaacagtgatgagcaaatcggaaatcgacatga 393  
 QY 380 aacaagtataaagaagatcttggttcatattttcaagtccaacaagcattttga 439  
 DB 394 aagatctaaacaacaactagctgctgtcagtttaactg---aactgagtggtgagc 450

QY 440 aggttaagacaatatgtgtgacgtgatcatcaagaagaaagatgtttagaagatcga 499  
 DB 451 agccggagaatataatgtgtgacgtgatcatcaagaagaaagatgtttagaagatcga 510  
 QY 500 ctagaagctactctggggaaccccaagtcacccgatttgggagtaggagcatagta 559  
 DB 511 ctagag---aggaaggagactagaagatgtgtcattcgtlaaggaaggaagcatcggga 567  
 QY 560 aacacaccttgaataaagaagattcaatgaatgaatcaatctatgctcgttttgatc 619  
 DB 568 aacaaccttggctacaacactctatagtcacgctgcatattgtctggtttgataatc 627  
 QY 620 atgcttgggtctacatctcacaagcacacaataaagaagaaatltgtggtccttgc 679  
 DB 628 gtgcacaagaacatttcaacaagatattgtgtgaatgatactccctagcctctt 687  
 QY 680 attcacaataaataatgataaggttaagaatgtttggaagcagagctgacagaca 739  
 DB 688 ctltgacaagtatgacactgtal-----gatacgtcagcggacc 726  
 QY 740 tgttacaagaagatttaagaagaaggtactaattgtctgtgataatctgagtt 799  
 DB 727 gactgcaaaagacatctgaaagcagagagataactgtgtatgcatctgatacatgtgaca 786  
 QY 800 gtgaagtgtggaatggtgagagacgtgtcttccaactgaaagacaatgcaaggagtcgaa 859  
 DB 787 cagaagcttggagatgataaaactatgttccacagactgtataat---ggaagcaga 843  
 QY 860 tactgttgcataccgtaataatgataagtgatgtgtatgtgtgtgtagaagattttct 919  
 DB 844 tactcctgactactcgaatgtggaagtgtgaaatgtgaaatgtgaaatgtgaaatgtgaa 903  
 QY 920 ttggagtgagactatggaatcaagatgagagtggtgagctcttcaaaagtgcagacatt 979  
 DB 904 atcactgtgcctccatgaaatttggagaaagtggaatttactacaacaagaactcttg 963  
 QY 980 caagtgaag---catacatatgagctgcagactgttggaagcaaatgcagagatgaat 1036  
 DB 964 aaaaagaagttcttcttccctgaatttgaataatgtggaacaacaatgtcattaaat 1023  
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 DB 1024 gtggagatgaactcctcagcaatlaactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1083  
 QY 1094 caataagaatgtgaaactgtgtctaaagatgtaacagtcattcgtlacaacaatgtact 1153  
 DB 1084 gattagatgagtgcaagaagattgtgggaataatgaaatgtgtgtgtgtgtgtgtgtgt 1143  
 QY 1154 atgaacgattgtcaagtgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1213  
 DB 1144 aagcacaatgcatgagagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1203  
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 DB 1204 cgtgttctgtatcttgcgaatttccacaaggttgtaacagatttcgttaatagaact 1263  
 QY 1274 tgaatcatgatacgtctgaggtgtcctga-----agtgtgaataatgatttggagag 1327  
 DB 1264 ttgattatgtcctgtatgagaggttttttgatgaagaagaggggaagaagcatagaag 1323  
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 DB 1324 tggcaacaacatgtatlaaagaaacttataagtaagacttaattttlcatccacaattt 1383  
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 DB 1384 gtttctgtgaacaacatgaaag---ttgtggaatgagtgatgtgacccgtgaactcgtt 1440  
 QY 1448 tgaagaagtccaagggagaaacattt 1477  
 DB 1441 tgaaggagagctcgaaacatgaatttltga 1470



Db 1319 tggcaacaacatgtataaagaactatagatagaagcttaatttcacacaaatttta 1378  
 Oy 1388 gtccagatgtgaacaaataatgacatgtaaggttcacatctatatatgaactgtgcg 1447  
 Db 1379 gtcttcgtggaacacataagaag---ttgtggaatgcatgtgtgacccgtgaactcgtt 1435  
 Oy 1448 tggagagaagttcaaaaggagagaacttttta 1477  
 Db 1436 tgaaggagaagctcgaaacataatcttctga 1465

RESULT 15  
 AAS03719  
 ID AAS03719 standard; cDNA; 2885 BP.  
 AC AAS03719;  
 DT 29-AUG-2001 (first entry)  
 DE DNA encoding Rx 32, a modified resistance protein.  
 XX  
 KW Rx; modified resistance; NBS; LRR; cell death; autoactivator;  
 KW nucleotide binding site; leucine rich repeat; pathogen resistance;  
 KW plant; ss.  
 XX  
 OS Solanum tuberosum.  
 OS Synthetic.  
 FH  
 FT Key Location/Qualifiers  
 FT CDS 37-2850  
 FT /\*tag= a  
 FT /product= "Modified resistance protein 32"

XX MO200129239-A2.  
 PN 26-APR-2001.  
 PD 12-OCt-2000; 2000WO-GB03930.  
 PF 15-OCt-1999; 99GB-0024483.  
 PR (PLAN-) PLANT BIOSCIENCE LTD.  
 PA Bendahmane A, Baulcombe DC;  
 PI  
 XX WPI: 2001-290924/30.  
 DR P-PSDB; AAU02149.  
 DR  
 XX  
 XX Modifying activation characteristics of plant resistance proteins to  
 PT produce autoactivator polypeptide capable of activation in absence of  
 PT elicitor, by introducing modifications in amino acid sequence of  
 PT protein -  
 PS  
 PS Disclosure: Page 46-57; 77pp; English.

XX The sequence represents the coding sequence of Rx clone 32, a modified  
 CC resistance autoactivator. Rx encodes an NBS-LRR polypeptide having a  
 CC nucleotide binding site (NBS), leucine rich repeat (LRR), and which  
 CC mediates cellular response leading to pathogen resistance and/or cell  
 CC death or dysfunction in response to an elicitor. The Rx was modified by  
 CC introducing modification to the amino acid sequence to produce an  
 CC autoactivator polypeptide, capable of activation in absence of an  
 CC elicitor. Decoupling of resistance response from its natural elicitor is  
 CC useful for developing novel pathogen resistant plants. The modified  
 CC resistance proteins are useful for conferring resistance to non-natural  
 CC agents or stimuli and also for investigating resistance response pathways  
 CC and protein interactions e.g. with activators and repressors.  
 CC  
 CC  
 CC Sequence 2885 BP; 861 A; 514 C; 649 G; 861 T; 0 other;

Query Match 9.8%; Score 266; DB 22; Length 2885;  
 Best Local Similarity 54.7%; Pred. No. 4.5e-61;

Matches 724; Conservative 0; Mismatches 555; Indels 45; Gaps 8;  
 Oy 166 gttttggggaagagacggattttgaagtagaggaaggaagttgcaggtcgtcgaa 225  
 Db 175 gatactgggggttaacaactcttggaattgaatcgtgaagggtgagcctaacacagcaga 234  
 Oy 226 tacacattcaacttgaagctaacaggaactgtactggaagaaataaaagccagaanaa 285  
 Db 235 gatactgttgcctcggaatcaagaatgttttttagcacgaatttggaggaagaagc 294  
 Oy 286 aagcgcgtcgaaggttcgtcgaagccttcgaacagtagcagaagagatgatcatc 345  
 Db 295 aggcgtatgttggaagattgttctgcctcctggaacagactagaatgtatgtatccccc 354  
 Oy 346 tggaaagagtcgacaaagatccaaagataaagaaacaagttacaaagatcatgtgtt 405  
 Db 355 gtgaacacagttgagtgacacatcgacgcgcgtgaagaatctcaaacccagaaactgcgcg 414  
 Oy 406 catgattttcaagttcacaaacagatatttgaaggttaagaacataatgttgagcgt 465  
 Db 415 ctgtcgttttaacctgaa---catgattgtgacgaccccggaataataatgttgcgcgt 471  
 Oy 466 gatgataaaggaacagttgttagaagatcgtactagaagctactctggygaaccocaa 525  
 Db 472 gaaatgtaattgagatgtgtgtgatacactgtcgtcagaagagggaa---gggaactgaa 528  
 Oy 526 gtcatcccgattgtcggatggaagcagataggttaaacacaccttgacaaagaattac 585  
 Db 529 gtgtcctcaatcgtatgagatggaagcgtcgggaacaaacttgcgtacaaactctat 588  
 Oy 586 aatgataatcaattctatgcggttttgatgtcgtacgtcgtggtacatctcaacag 645  
 Db 589 agtgcctcgtgattatgtctcgtatgtatctgtcgaagaagcaactgttccacaagaag 648  
 Oy 646 caacaacaaaggaattttgttcggccttcgtcgtcgtcgtccacatcaaaatgtgatcag 705  
 Db 649 tatgtgtgagaagagttcctcctagcgtcttcttcttgacaagatgtaacctgat--- 705  
 Oy 706 gtttaagatgtgtgtgaagcagaagctagcagacatgttcaagaagaagtttaagaagaag 765  
 Db 706 -----gatcagctagggagccgactgcaaaagcatctgaaagcag 747  
 Oy 766 aggtacttaattgtcttgatgatatctggaagttgtgaagtgtggatgtgcgtgagcga 825  
 Db 748 agatacttgtagcatgtgatacatatgactacagaaagcttggagatgataaaacta 807  
 Oy 826 tgccttccaaacgaagacatgcagggagtcgaatactgtgacacccgtaattgtga 885  
 Db 808 tgtttccca---gactgtataatggaagcagaatactctcgtactcctcgaaatgtggaa 864  
 Oy 886 gtagctgttactgtgtgtgtagaagattttcttcttgagatgagttcatggtatcagaat 945  
 Db 865 gtgcgtgaatagctcagttcaggttaagcctcctcatcacatcgcctcgaattttgac 924  
 Oy 946 gagagttgagtcctttcaaaagttgcagcattttcaagtgaag---cattacatattgag 1002  
 Db 925 gaaagttggaattacttaacaaagaatcttgaagaagaagtgatttattcttcctgaa 984  
 Oy 1003 ttcgagactgtggaagaagaatcgcagatgaatgtgcaggggttaccacataactgtgc 1062  
 Db 985 ttggaataatgtggaacaaatgtgataaaatgtgggggattactactctagaataact 1044  
 Oy 1063 gtgtgtcagggcctct---caaatcaaaaggaacataatggaagattggaacactgtgct 1119  
 Db 1045 gattgttcggagactcttcacaaatgtggccaagaatagatgatyggcaagaatggg 1104  
 Oy 1120 aagaatgtcaatgtcgttcacaaatgttcctgataagacagatgttcaggtgtgctgg 1179  
 Db 1105 gaaaatgtaagtcgtgcgttcagacagatcccggaagcacaatgcatgagatgtgtgct 1164  
 Oy 1180 ttgagttacagatcactgtgcaagcgaatctaaacacatgtcttcgtacttgcgaatttt 1239  
 Db 1165 ttgagttacatcactgtgcctctcaacctaaaccggtttctgtatattgaactttc 1224



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 11, 2002, 19:26:02 : Search time 6528.21 Seconds  
(without alignments)  
5619.415 Million cell updates/sec

Title: US-09-864-680-4  
Perfect score: 2718  
Sequence: 1 atggcgtatgcaagtgctgc.....ctgattcagaagaacattag 2718

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 13736207 segs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :  
EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	145.2	5.3	663	10	BI433950 EST536711
2	135.4	5.0	535	10	BM109555 EST557091
3	135.4	5.0	691	10	BI406780
4	135.2	5.0	635	9	AW979731
5	126.2	4.6	669	10	BM411546
6	125.4	4.6	607	10	BE473157
7	122.2	4.5	659	10	BE1934806
8	120.4	4.4	426	10	BE923412
9	119.6	4.4	701	12	AO367206
10	118	4.3	515	10	BI934083
11	118	4.3	639	12	BI143383
12	113	4.2	617	10	BE460726
13	108.4	4.0	756	10	BM408141
14	107.2	3.9	417	9	AW030063
15	105.4	3.9	660	9	AW216532
16	104.8	3.9	524	12	BI142479
17	103.4	3.8	576	9	AT772710

18	102.8	3.8	464	10	BF114223
19	100.6	3.7	579	9	AM034628
20	100.4	3.7	573	10	BM407382
21	100.2	3.7	643	9	AM622905
22	98.8	3.6	558	10	BF053416
23	98	3.6	558	10	BI425924
24	97.2	3.6	593	10	BM110993
25	97	3.6	800	10	BI421945
26	96.4	3.5	779	10	BG596578
27	95.2	3.5	526	9	AM217536
28	94.8	3.5	587	9	AM934420
29	94.4	3.5	323	9	AM933105
30	90.8	3.3	725	9	BI177939
31	90	3.3	339	10	BI176878
32	89.8	3.3	414	9	AW737247
33	88.8	3.3	784	10	BI432845
34	83.8	3.1	604	10	BI179578
35	81.8	3.0	785	10	BM404923
36	81.2	3.0	686	10	BI920482
37	81.2	3.0	692	10	BI920471
38	81.2	3.0	708	10	BI920408
39	80.8	3.0	541	10	BM178803
40	80.8	3.0	606	10	BM405792
41	79.8	2.9	663	10	BG890386
42	79	2.9	471	10	BF054511
43	78.8	2.9	555	9	AM737464
44	78.6	2.9	433	9	AM031596
45	78.4	2.9	396	10	BM409153

## ALIGNMENTS

RESULT 1  
BI433950  
LOCUS  
DEFINITION  
PCBR40 5' sequence, mRNA sequence.  
ACCESSION  
BI433950  
VERSION  
BI433950.1 GI:15258640  
KEYWORDS  
EST.  
SOURCE  
ORGANISM  
Solanum tuberosum  
potato.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

REFERENCE  
1 (bases 1 to 663)  
Restrepo, S., Griffiths, H.M., Smart, C.D., Cho, J., Chieningo, A., Bougri, O., Buell, C.R., Romling, C.M., Fry, W.E., and Baker, B.

Generation of ESTs from Potato Leaves Challenged with Phytophthora infestans, Compatible Interaction  
Unpublished (2000)

JOURNAL  
COMMENT  
Contact: Cathy Romning  
The Institute for Genomic Research  
For clone info: please contact Research Genetics, Libraries  
Division tel 1-800-711-6195, email cdna@resgen.com  
Seq primer: MJ3F-R.  
Location/Qualifiers

FEATURES  
source  
1.663  
Location/Qualifiers

/organism="Solanum tuberosum"  
/cultivar="Kennebec"  
/db\_xref="taxon:4113"  
/clone="PCBR40"  
/clone.lib="P. infestans-challenged leaf"  
/tissue\_type="leaf"  
/dev\_stage="6 week old"  
/note="Vector: pBluescript SK(-); Site.1: EcoRI; Site.2: XhoI; Whole plants were challenged with 450,000 sporangia/ml P. infestans US-1 (DS 940501) in Biotron (Madison, Wisconsin). Leaf tissue was collected at 1, 2, 5, 12, and 24 hours post-challenge and frozen in liquid nitrogen immediately upon removal. Kennebec plants showed





[illegible]

QY	2654	accctgtgagtttgcgtatctccaatccatctgaagga	2690
Db	540	ACATACCTCAACTTATGCTATGACACATTTAGAGA	576
RESULT	4		
LOCUS	AM979731	635 bp	mRNA
DEFINITION	EST341354 tomato root deficiency		linear EST 18-MAY-2001
ACCESSION	AM979731	esculentum cDNA clone CLEM8H19 5'	Cornell University Lycopersicon
VERSION	AM979731.1	GI:8171253	
KEYWORDS	EST.		
SOURCE	tomato.		
ORGANISM	Lycopersicon esculentum		
REFERENCE	1 (bases 1 to 635)		
AUTHORS	van der Hoeven,R.S., Garvin,D.F., Matern,A.L., Holt,I.E., Liang,F., Upson,J., Hansen,T.S., Roming,C.M., Craven,M.B., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,U.C., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.		
TITLE	Generation of ESTs from tomato nutrient-deficient roots		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: CUGI		
	Clemson University Genomics Institute		
	Clemson University		
	100 Jordan Hall, Clemson, SC 29634, USA		
	Email: <a href="http://www.genome.clemson.edu/orders/index.html">http://www.genome.clemson.edu/orders/index.html</a>		
	5 prime sequence.		
FEATURES			
SOURCE	Location/Qualifiers		
	1. 635		
	/organism="Lycopersicon esculentum"		
	/cultivar="TA496"		
	/db_xref="taxon:4081"		
	/clone="CLEM8H19"		
	/clone_lib="tomato root deficiency, Cornell University"		
	/tissue.type="roots"		
	/dev_strage="5-6 weeks old"		
	/note="vector: pBluescript SK-; Site_1: 5' EcoRI; Site_2: 3' XhoI; supplier: Tanksley; tissue supplied by Dave Garvin (USDA-ARS, Ithaca, NY 14850). Roots were harvested from plants grown under the following		
	deficiencies/stresses: 10 mM Al, Zn, P, K, Fe, N), and mRNA was isolated from individual treatments. Proportional aliquots of mRNA of each treatment were mixed and used for library construction."		
BASE COUNT	200 a	99 c	163 g
ORIGIN		173 t	
Query Match	5.0%;	Score 135.2;	DB 9; Length 635;
Best Local Similarity	54.7%;	Pred. No. 6.3e-21;	
Matches 338;	Conservative 0;	Mismatches 268;	Indels 12; Gaps 3;
QY	452	ataatgttggaagcgtatgatcaagaagaacagctttagaagaatcgtactagaagctact	511
Db	30	ATAATGTGGGTTTGGGANTGACATRAGAAAATGTTTCATGATCTGATTAGAGC---TA	86
QY	512	ctggggaaccccaagatcattccgatttctgggagatggaagcagtgtaaacacacttag	571
Db	87	CAAAATGATCTACAGCTGTGTCACCAATGTGATGGCATGGGTGGACAAAGGAAACGACAGTTG	146
QY	572	caaaagaagtttacaatgatgaatcaatctatgccgttttgatgttcaatgccttggcta	631
Db	147	CTAGGAAGGCTTACACATATAGTGACAACATGTGTTTCATTTGATGTCGAGCATGGTGCA	206
QY	632	catatctcaagaagacacaaaagaagaattttctgggccttcgtcagttccacaatca	691
Db	207	TGCTTTCCCAACATATATACCGGAGAGAACTTTTACAGACATTTTGAATCAAGTTACC-	265

Oy 692 aaatgtagacagggcttaagatgatgtgtgaagcagagctgcagacaacttaacaga 751  
 Db 266 -----GTTTCCAGGACACAAGGGGTTAGAGATGATATCTCTGTATGATGAGGAAAA 320  
 Oy 752 gtttaagaagaagaaggtacttaattgtcttggatgatatactggaattgtgaagtgtgg 811  
 Db 321 GCTTAATGAGGCAAGAGATATCTCATTTGCTTGATGATATGAGGATGTATGATGATGAGG 380  
 Oy 812 atggcgtgtagacgatgctttccaactgaaagacaatgcagggaggtcgaatactgttgacta 871  
 Db 381 AMGACTTTAAGGCTTTCCCTTCCAGATTCCGGAATAAGAGCA--GAATAGTAGTAACAA 437  
 Oy 872 ccccgatgaatgaatgaatctgttgtatgctgtgtgtagagaatttcttcttgcsyagagct 931  
 Db 438 CTCGACTTGAGAAATGGGCCACAGTCACATCACTGATCTCTTAATTTCTTCCGT 497  
 Oy 932 tcatgatacaagatgagagttgagcttcttttcaaaagtgcagcatttccaagtgaagcat 991  
 Db 498 TCCCTACAAAAGAAAGAGAGTGTGTAATTGTTCAAAAAAAAGTGTTTAAAAAGGAAGATT 557  
 Oy 992 taaccaatgaagttcgagagactgttgaagaagcaaatgcacagatgaatgtcaaggyttaaccac 1051  
 Db 558 TCCCCCTCGAACATACAAAGATGTGAGTCCAGAGCAGTGTGCAGAAAAAATGCAAAAGGACTGCCCC 617  
 Oy 1052 taactatgtcgtgtg 1069  
 Db 618 TAGTGTTGTCTCTTGSGGTG 635

RESULT	5
BW411546	
LOCUS	BW411546
DEFINITION	669 bp mRNA, linear EST 22-JAN-2002
	E8758873 tomato breaker fruit Lycopersicon esculentum cDNA clone
	CLEG57I23 5' end, mRNA sequence.
ACCESSION	BW411546

VERSION	BM411546.1	GI:18263176
KEYWORDS	EST.	
SOURCE	tomato.	
ORGANISM	Lycopersicon esculentum	

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 669)  
Alcala,J., Vrehlov,J., White,R., Vlsion,T., Karamycheva,S.A., Tsai  
,J., Bougri,O., Kirkness,E., Utterback,T., Van Aken,S., Roming  
,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D., and Giovannoni,J.  
Generation of ESTs from tomato (Lycopersicon esculentum) cDNA  
Unpublished (2002)  
Contact: CUGI

FEATURES	Location/Qualifiers
source	1. .669

/note=Vector: pBluescriptSKmCnaadpl; site\_1: EcorI; site\_2: XhoI; supplier: Boyce Thompson Institute; sequencing: The Institute for Genomic Research. Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of fruit). Fruits were cut in half and the seeds and locules were discarded

BASE COUNT	187 a	119 c	136 g	227 t
ORIGIN	prior to freezing the pericarp.			

Query Match	4.6%	Score 126.2	DB 10	Length 669
Best Local Similarity	55.6%	Pred. No. 7.9e-19		
Matches 242	Conservative	0	Mismatches 193	Indels 0
				Gaps 0

[illegible]

Db 143 GGATCTCGGTTTCATTTGGAGGAGATTTTGGAGATTCCTTGGTAAATTTGCCCTAAATCTCGAGGCC 202

Dbb 203 CTTAACTAGCATATGATGCCCTGCATGCTACTGATTCGGAGACTAGTGAACAGCCTTT 262

Db 263 CCACACTTTGAGACATCTTTCGGATTGACGATTATATCTTCGACATAGATGATACCTAGATGT 322  
 2479 aacaaattttccctatccctttaaagccctcatgaattttaaagatctgcaaaaatttggaaaagata 2538

Db	323	GATCACCTTCCATGCGCTTGAACGACCTAGTCAATTAACCGTGTGGACCATGTATTTCATC	382
QY	2539	cccatltagtlttgcagatatcacacacactacagctgattgattlaagagagtgctctcc	2598

Db	383	CCACAGACATTGTAGACATAACCACTCTTTCAGCTGATTCAGTAACTGACTCTGCAAA	442
Qy	2559	aaacttgggaattctgtctcaagaattcgaagaagacaagaagaccccgaaacaaacct	2658

2659 gtagatgctgatac 2673

## RESULT 6

LOCUS	BE474315/	60/ dp	mRNA	linear	EST 28-JUL-2000
DEFINITION	BT4148010 potato stolon, Corni University Solanum				
ACCESSION	clone cSTFA3606, mRNA sequence.				tuberosum cDNA
	BA73157				

KEYWORDS	EST.
SOURCE	potato.
ORGANISM	Solanum tuberosum

REFERENCE  
 1. (bases 1 to 607)  
 1. (bases 1 to 607) *Percepsidae* I. Pachow C. Horowitz B. Wiegand  
*Percepsidae* I. Pachow C. Horowitz B. Wiegand

**TITLE**

Generation of ESTs from potato swelling stolons  
B.  
'B, Bougri, O., Buell, C.R., Romling, C.M., Tanksley, S.D. and Baker  
HOLC, L.E., Zhang, P.L., Hansen, K.S., Gschwendt, J., Beck, C.B.  
'B, Bougri, O., Buell, C.R., Romling, C.M., Tanksley, S.D. and Baker

COMMENT

Contact: Research Genetics, Libraries Division  
Tel: 1-800-711-6195  
Email: [cdna@resgen.com](mailto:cdna@resgen.com)

```
FEATURES
source
location/Qualifiers
1. .607
/organism="Solanum tuberosum"
/cultivar="Bintje"
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./clone_lib="potato stolon, Cornell University"
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Y	1333	gagaaggttttcgaagcctgttcgatgatgatgtctatctatcccttcgttcgaagcagaaggaagtcga	1392
Db	470	-----ATTGTATGAGAGATCTTGTATGCGAGGATCTGGTAATGTTTGAAGAAACGAGGATTTT	525
Oy	1393	gatggaacaaaatatagatcattgaaggttcattgatctataataatgatccgtgtgcgtgaga	1452
Db	526	AATGC---CGAGACACAAAACATGTGTGTGTCATGCAATCGATTCGTGATTTGATTTTAAGA	582
Oy	1453	gaagttcaaggagaga	1469
Db	583	AGAGCCGAGAAAGAGAA	599
RESULT	8		
LOCUS	BE923412	426 bp	linear
DEFINITION	EST427181 potato leaves and petioles Solanum tuberosum cDNA clone		
ACCESSION	BE923412		
VERSION	BE923412.1		
KEYWORDS	EST.		
SOURCE	potato.		
ORGANISM	Solanum tuberosum		
REFERENCE	1		
AUTHORS	van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J., uterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning , C.M., Fry, W.E., Tanksley, S.D. and Baker, B.		
TITLE	Generation of ESTs from potato leaves and petioles		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Cathy Ronning The Institute for Genomic Research For clone request: please contact Research Genetics, Libraries Division tel 1-800-711-6195, email cdna@resgen.com.		
FEATURES	source		
	1..426		
	/organism="Solanum tuberosum"		
	/cultivar="Kennebec"		
	/db_xref="taxon:4113"		
	/clone="cSTB24L4"		
	/clone_1lb="potato leaves and petioles"		
	/tissue_type="leaflets and petioles"		
	/dev_stage="8 weeks old plants"		
	/lab_host="SOLR"		
	/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Tissue was supplied by Dr. Fry (Cornell University). Leaflets and petioles were isolated from 8 week old greenhouse grown plants. The plants were watered and fertilized freely. The tissue was immediately frozen in liquid nitrogen."		
BASE COUNT	130 a	76 c	102 g
ORIGIN			118 t
Query Match	4.4%;	Score 120.4;	DB 10; Length 426;
Best Local Similarity	58.5%;	Pred. No. 1.7e-17;	
Matches	261; Conservative	0; Mismatches 161;	Indels 24; Gaps 2;
Oy	514	ggggaacccaagatcccgatgtcggatgggagcatagttaaacacacttagca	573
Db	1	GGGGACATAGAAATGTGTCAATCGTAGGAGATGGAGCGCATCGGAAACAACATTGGCT	60
Oy	574	aaagaagttcaatgatgaatcaaatcttaatggcgtttgttcattgcctgggtacc	633
Db	61	ACAAACTCTATAGTATCTGTGCATATAGTCGATTGATTCGTGCAAAACCAACT	120
Oy	634	atatccaacagcaacaaaagaatttgcctggcgcttcgtcaccacaatca	693
Db	121	GTTTCACAAAGATATTGTGTGGAATATGTACTCCAGAGCCTTTCTTTTGACAAAGTGAT	180
Oy	694	atgatgcagggttaagatgatgtgtgaagcagaagctagaacatgttacaagaaagt	753

Db	181	GAACTGATA-----ATCAGCTACGCGACCGACTGCAAAACGAT	219
QY	754	ttaaagaagaaggtacttaatttcttgatgatgatcctggagttgtgaagttgagat	813
Db	220	CtGAAGAGCGAGAGACTTGGTACTGATCTGATGTGACATATGACATACAGAAAGCTTGGAT	279
QY	814	ggcgtgagacgctgtcttccaacctgaagaacaatgcagggagtcgaatactgttgcacc	873
Db	280	GATATATAAACTATGTTTCCCA---GACGTATATATGAGACAGAGATATCTCTGACTACT	336
QY	874	cgtaatgatgaagtagctgtgtatgctgcggtgtagaagaatttcttgcgagtagcttc	933
Db	337	CGGATGTGGGAAGTGGCGAATATCTGTATTCGAGTAAGCCTCTCATACATGCGGCTC	396
QY	934	atgagatcaagatgagagttggagctc	959
Db	397	ATGAATTTTTCAGCAAAAGTTGGAATTT	422
RESULT	9		
LOCUS	A0367206	701 bp	DNA linear GSS 07-MAR-2000
DEFINITION	tox00002A12r CUG1 Tomato BAC library Lycopersicon esculentum		
ACCESSION	A0367206		
VERSION	A0367206.1	GI:4221674	
KEYWORDS	GSS.		
SOURCE	tomato.		
ORGANISM	Lycopersicon esculentum		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.		
AUTHORS	1 (bases 1 to 701)		
TITLE	Budiman,M.A., Mo,L., Wood,T.C. and Wing,R.A.		
JOURNAL	A deep-coverage tomato BAC library and prospects toward development of an STC framework for genome sequencing		
MEDLINE	Genome Res. 10 (1), 129-136 (2000)		
COMMENT	201113122		
CONTACT	Wing RA		
INSTITUTION	Clemson University Genomics Institute		
ADDRESS	Clemson University		
LOCATION	100 Jordan Hall, Clemson, SC 29634, USA		
TEL	Tel: 864 656 7288		
FAX	Fax: 864 656 4293		
EMAIL	Email: rwing@clemson.edu		
SEQ PRIMER	Seq primer: GGAACACGCTATGACCATG		
CLASS	Class: BAC ends		
FEATURES	High quality sequence stop: 387.		
SOURCE	Location/Qualifiers		
	1..701		
	/organism="Lycopersicon esculentum"		
	/cultivar="Heinz 1706"		
	/db_xref="taxon:4081"		
	/clone="tox00002A12r"		
	/clone_id="CUG1 Tomato BAC library"		
	/tissue-type="Nuclei preparation from leaf"		
	/lab_host="E. coli DH10b"		
	/note="Vector: pReloBAC 11. Site_1: HindIII, Site_2: HindIII; Tomato is a vegetable crop that ranks second only to potatoes in value and importance. Among plant geneticists and physiologists, tomato represents an ideal dicot model beside Arabidopsis and monocot rice to derive genomic information from. To facilitate the genome analysis of tomato, we have constructed a tomato BAC library that is suitable for positional cloning, physical mapping, and genome sequencing. The library contains 129 ,000 clones and a random sampling of 498 clones indicated an average insert size of 117.5 kb. With 15x haploid genome equivalents (1C equals 953 Mb) (Arumuganathan and Earle, 1991), the probability to recover any particular sequence is greater than 98%. High stability, large insert		

and ease in manipulation make BAC libraries the choice for genome sequencing. Pre characterization of a few hundred bases of insert ends will make BAC clones extremely useful for rapid contig assembly (Venter, Smith, and Hood, 1996). Here we present the construction, characterization of the tomato BAC library, and preliminary analysis of the 1536 tomato BAC end sequences."

BASE COUNT 214 a 101 c 182 g 204 t  
ORIGIN

Query Match 4.4%; Score 119.6; DB 12; Length 701;  
Best Local Similarity 53.6%; Pred. No. 2.8e-17;  
Matches 295; Conservative 0; Mismatches 249; Indels 6; Gaps 2;

Qy 759 gagaaagaggaactaatgttcttgatgatactcgtgagtttgaaagtgtgagatgagcgt 818  
Db 4 GGGCAAGAGATATCATCTGATGCTTGGATGATATGCGATTGTATGCGATGGGATGACTT 63  
Qy 819 gagacgatgcttccactgaagacatgcagggagtcgaactgttgaactaccgttaa 878  
Db 64 AAGGCTTCCTTCTCCAGATCCGGAATATGAAAGCA---GAATAGTAGTAACTCGACT 120  
Qy 879 tgatgaagtagctgttactgtgtgtgtagaattttcttcgagatgagcttcagtga 938  
Db 121 TGAGAAAGTGGCGCAAGCAAGTCAGTACGATCCTATTCCTTCCTCCTCAC 180  
Qy 939 tcaagatgagaggttgagatcttttcaaaagtgcagcatttccaagtgaaccata 998  
Db 181 AAAAGAAAGAGTGTGATGATGTTGCAAGAAAAGTGTTCAAAAGGAAGATTCCTCCGC 240  
Qy 999 tgaagtcagagctgttgaaagcaaatgcagatgatagttcacgggttaccactaat 1058  
Db 241 TGAAGTAAAGATGTGATGATCCAGAGTTCGCAAAATGCAAGAGACGCTCCCTAGTGT 300  
Qy 1059 tgcgtgtgtcaggggttctcaaatcaaaagcaatgagaatttgaaactgttgc 1118  
Db 301 TGTCTGTGACTCGAATATCAAAAAAGCAAAATGAGAGATCTGTGATGAGAGT 360  
Qy 1119 taaagatgcaagtcattctgcacaaa---tgatcctgataagcagatgttccagtgct 1175  
Db 361 GAAAGATCTTATTTATTTGACCACTTATATCGTAGTCGGAAGAAATVATCTTTCAACTAT 420  
Qy 1176 tgggttgatgacatcactgacaaagcagatcctcaaaacatgtcttcacattcgagt 1235  
Db 421 GCAGTGTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 480  
Qy 1236 ttcccaagaagcagtgatattccagtgagaagtgttgatgacatgagtgagtgag 1295  
Db 481 GTTTCAGGAGGATGCAATTAATTCGAGTATCTGAATTTGATGATGATGAGATTGGCGAG 540  
Qy 1296 gttcctgaag 1305  
Db 541 GATTTGTGCGAG 550

RESULT 10  
BI934083 515 bp mRNA linear EST 18-OCT-2001  
LOCUS  
DEFINITION  
EST353972 tomato flower, anthesis Lycopersicon esculentum cDNA  
clone cTOD18D10 5' end, mRNA sequence.  
ACCESSION  
BI934083  
VERSION  
BI934083.1 GI:1624855  
KEYWORDS  
EST.  
SOURCE  
tomato.  
ORGANISM  
Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asteridae; euasterids I; Solanales; Solanales; Solanaceae; Solanum;  
Lycopersicon.  
1 (bases 1 to 515)  
van der Hoeven, R.S., Bezzerides, J.L., Karamycheva, S.A., Tsai, T.,  
Uiterback, T., Van Aken, S., Ronning, C.M., Nierman, W., Fraser, C.M.,

TITLE  
JOURNAL  
COMMENT  
Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.  
Generation of ESTs from tomato flower tissue, anthesis (2001)  
Unpublished (2001)  
Contact: CUGI  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Email: <http://www.genome.clemson.edu/orders/index.html>  
This clone is available through the Clemson University Genomics  
Institute  
Seq primer: 73.

FEATURES  
source  
Location/Qualifiers  
1..515  
/organism="Lycopersicon esculentum"  
/cultivar="TA496"  
/db\_xref="taxon:4081"  
/clone="cTOD18D10"  
/clone\_11b="tomato flower, anthesis"  
/tissue="flower"  
/dev\_stage="anthesis"  
/note="vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI; supplier: Cornell University; sequencing: The  
Institute for Genomic Research; Flower buds and flowers  
were taken from greenhouse plants (4-8 wks old, TA496).  
They were immediately frozen in liquid nitrogen and then  
size-separated while remaining frozen."

BASE COUNT 157 a 77 c 121 g 160 t  
ORIGIN

Query Match 4.3%; Score 118; DB 10; Length 515;  
Best Local Similarity 58.7%; Pred. No. 6.3e-17;  
Matches 262; Conservative 0; Mismatches 175; Indels 9; Gaps 3;

Qy 859 atactgtgactaccgtaatgataagtagctgttactgtgtgtagaagattttct 918  
Db 1 ATTATTTTGGACTAGTAGGCAAGAGAGTGTCTAGTCATGACAGATCTGATGCAATCT 60  
Qy 919 ttgcgagtagcttcatgataagatgagatgagatgagcttccaagaatgagcatt 978  
Db 61 CATAAATGAACTCTTAACTTGGATATATGATGGAATTAATCCGTCAGAGAGTGT 120  
Qy 979 tcaagtga---gcatcacaatagatgagcagctgttgaaagcaatgcagatga 1035  
Db 121 GGGGTGAAGACATGATGCTCTCTGATGTGAGGATATGAGAACATATACACAAAGA 180  
Qy 1036 tgcacgggttaccactaactatgtcgtgttgtagagggctctc---aatctaaagg 1092  
Db 181 TGCCAAGAGACTGCTTGTAGCTTGTAGGTAGGCGGACATCTCTAAATTTCTAGA 240  
Qy 1093 acaatagaagatggaagaactgtgctaaagatgcaagtcatttgcacaatgct 1152  
Db 241 ACACGAGAAAGTTGAGACAGATGTTCCAAAAGTGAATGAATGATGTTGCTGATGAATGA 300  
Qy 1153 gatgaagatgttcagctgtgtgttgatgataagcatttcgaagcagatcctaa 1212  
Db 301 GAT---ATATGCTAGAGAGTGTCTGCTATGATTAACATTAATTAATTAATTAATTAAT 357  
Qy 1213 acatgtctctgacattcggaaatttccagaagaagcagtgatcctcagtgagaatttg 1272  
Db 358 CCATGTTTCTTACATGAGTGTGCTTCCGGAAGACAGTGTGTTAACATTTGATGATTG 417  
Qy 1273 atgagatcagatgagtgaggggt 1298  
Db 418 ATCAACTTATGAGATTCTGAGGGTTT 443

RESULT 11  
BH142383 639 bp DNA linear GSS 16-AUG-2001  
LOCUS  
DEFINITION  
T06D021TH cT0G Lycopersicon esculentum genomic clone cT0624C17, DNA  
sequence.  
ACCESSION  
BH142383

VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	TITLE	JOURNAL	COMMENT	FEATURES
B54.2383.1	GI:15194909		tomato.					
			Lycopersicon esculentum					
			Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;					
			Lycopersicon.					
			1 (bases 1 to 639)					
			van der Hoeven,R., Sun,H., Cho,J., Utterback,T., Roming,C. and Tanksley,S.					
			Tomato Demethylated Genomic DNA Sequences					
			Unpublished (2001)					
			Contact: CUGI					
			Clemson University Genomics Institute					
			Clemson University					
			100 Jordan Hall, Clemson, SC 29634, USA					
			Email: <a href="http://www.genome.clemson.edu/orders/index.html">http://www.genome.clemson.edu/orders/index.html</a>					
			tomato demethylated genomic DNA					
			Insert length: 1270					
			Std Error: 0.00					
			Seq primer: M13P-R					
			Class: shotgun					
			Location/Qualifiers					
			1..639					
			/organism="Lycopersicon esculentum"					
			/cultivar="E6203"					
			/db_xref="taxon:4081"					
			/clone="CM0G24C17"					
			/clone_lib="cT0G"					
			/issue_type="young leaves"					
			/dev_stage="12-14 weeks post harvest"					
			/lab_host="E.coli JM109"					
			/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI. This library was made from short EcoRI digested fragments of the genome of Lycopersicon esculentum ligated into pBS (SK-). The fragments were cloned into the methylation restrictive E.coli strain JM109 with the purpose of enriching the library for non-methylated DNA fragments. This procedure may enrich the pool of cloned fragments in JM109 cells for sequences representing expressed genes. Average insert size 1.27 kb."					
			BASE COUNT					
			188 a 104 c 150 g 197 t					
			ORIGIN					
			Query Match					
			Best Local Similarity 4.3%; Score 118; DB 12; Length 639;					
			Matches 319; Conservative 0; Mismatches 285; Indels 10; Gaps 2.					
			868 actaccgctaagaagaagtagctgttaagctgtgtgtgtagagaattttcttgcgagatg					
			9 ACTGGCGTCAAGTATGTTGCTGATTATATGCAATGTCGCGTTTCGCCCTCATAGTAG					
			928 agcttcacatgatacaagaatgagagttggagctcttccaagaatgacgacatttcaagtga					
			69 TCTTCTTAAGCTCTGAAGATAGTTGGAATCATTTCCACCAAAAATTTATTCAAAAACAT					
			988 gattacacatagagattgagagactgtttgaaagcaaatgcgacgataagatgacagatta					
			129 CCGTGTCCCTCTCTTGAAAAAAGGGGGAAGCATATGTGAACAAATGTCGAGGATTA					
			1048 ccactaacatattgctgtgtgttcgagagctctccaatctcaaaagacaataagaagattgg					
			189 CCCCTCTCGGTGTGTGTTCTTCTGCTGAGACTGTGTGAAAAATGACCCACACATGATAT					
			1108 aaactgtgtcctaaagatgcaagtcacatgcgtccacaatgacatcctgataagcagattca					
			249 TGGAGAAGAGGTGTGAGGAAAAATCTGAGCTCGTCTTTGTGACGTGTCTCAACGATGCCAA					
			1168 cgt					
			309 TCAATTCCTTCTCTGAGCTACCAATTAATTTGGCCCAATATTATTAAGGCTTGTTTCTCTTAT					

QY	1228	tttggaaatttttcacgaagaacagtgatatccagtcgaagaatttgatgatgacatgagtg	1287
Db	369	gttgcagactttttcctgaagatgaggaattgattgtttccaaattgattggctatgagatt	428
QY	1288	gctgagaggggttcctgaaagttgaaatgat-----tggaaagagaggtttgagaagtgc	1341
Db	429	gcttgacgaatttctgaaaggcamaacaaattgaaagattggaagtgtgctggcagagagat	488
QY	1342	tgtgaagagagttgcatagatgctctagctccgtcgaagaagagtcgagatgaaaca	1401
Db	489	gttataaagatttaattgattacaaactctaaat---tttggctggtgaacaaaggcctaata	544
QY	1402	aaaattgatcatgctaaagttcattgataataatataatgacccgtgcgtgagagaagttaa	1461
Db	545	aggatgaaaaagttgcaaaaatttcacgattcttccgcaaatgtgcctaaaggcaactcaa	604
QY	1462	aggagagacatttt	1475
Db	605	actgaaaaattgtgt	618

RESULT	12
LOCUS	BE460726/c
DEFINITION	BE460726 617 bp mRNA linear EST 18-MAY-2001
ACCESSION	EST412145 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA
VERSION	clone GLEG36A22, mRNA sequence.
KEYWORDS	BE460726 BE460726.1 GI:9505028
SOURCE	EST.
ORGANISM	tomato.
REFERENCE	Lycopersicon esculentum Eunaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asterales; Asteridae I; Solanales; Solanaceae; Solanum;
AUTHORS	Lycopersicon. 1 (bases 1 to 617) Alcala,J., Vrehlov,J., White,R., van der Hoeven,R.S., Holt,I.E., Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M., Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley, S.D. Generation of ESTs from tomato fruit tissue, breaker stage Unpublished (2000)
TITLE	Contact: CUGI
JOURNAL	Clemson University Genomics Institute
COMMENT	Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Email: <a href="http://www.genome.clemson.edu/orders/index.html">http://www.genome.clemson.edu/orders/index.html</a> 5 prime sequence.
FEATURES	Location/Qualifiers
source	1..617 /organism="Lycopersicon esculentum" /cultivar="TA96" /db_xref="taxon:4081" /clone="GLEG36A22" /clone_id="tomato breaker fruit, TIGR" /tissue_type="Pericarp" /dev_stage="breaker" /lab_host="SOLR" /note="Vector: pBluescriptSMCdupat; Site_1: EcoRI; Site_2: XhoI; Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of the fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."
BASE COUNT	162 a 148 c 100 g 207 t
ORIGIN	
Query Match	4.2%; Score 113; DB 10; Length 617;
Best Local Similarity	51.1%; Pred.No. 9.5e-16;
Matches 291; Conservative 0; Mismatches 275; Indels 3; Gaps 1,	
684 cacacataaatgtagcagcggttttgtaagaagcctgcagcacatggt 743	

Db	586	CACCAATGGGAACCTAGGATTGTGGAAAAGAATGATGAAAGATCTAAGAAAAOCACC	527
OY	744	aagaagaattttaaagagaagaaggtaacttaattctgttgatgatcatcgtgaatttga	803
Db	526	TGCGTATCTATTTGAAAAGAACGCCAAATACCTTTGTGTGGTTGATGTGTCGCCAAAAGGA	467
OY	804	agtgtggatgctcgtagacagatgctttccaaactbaagacaatlgaagggaafgcgaatact	863
Db	466	MGCATGGGAGATTTTGAAAAGAGCATTCGCCGATPACAAGAAAT---GGCAGCAGAGTCAT	410
OY	864	gttgactaccocglaatgatgaagttagctgttatgtctggtgtgaagaaattttcttcgcg	923
Db	409	TATTATCCAGCGCCCAAGAGAGATGTGCTGTAAGAGACGCCGACAGATGTTTGTTTCATA	350
OY	924	gatgagcttcatalgatcaagaatlgagagatlgagatctttcaaagtltgaagcatttccaag	983
Db	349	ACTTGTTTTCCTAATGCAAGAAAGATGTGGATGCTCTTTCTTAGAAAACACTTGATGT	290
OY	984	tgaacattaccatatgattggttcgagacgtgttbgaaagcaaatcgcgaatgatatgtcaagg	1043
Db	289	TGCAGCAATGTGTGCAGAAATGCAAGTCCTACCTAAGGATATGTGTGAAGAACTGTAGAG	230
OY	1044	gttaccactaacattatgttcgtgtgtgccagggttcttcaaatctaagaagacaatagaaga	1103
Db	229	TTTACTCTTGCAATGTGTTGTATTGAGCGGAACTACTTTGCGATAAAAAGATCTGATGA	170
OY	1104	ttgaaaacatgttgttcaagaatgtcaagtcatactgtlccaaatgatactctgatgaagatg	1163
Db	169	ATGGCAAAAAGGTGAAGAATCACCTTTGGAGAAGCATTTAAAGAAATTAATCTGTGAAT	110
OY	1164	ttcaagtgctgtggttgatgattagatcacctgtgcaagcgatctctaaaaactgtctct	1223
Db	109	CTCCACAATACTATCACTTAAGCTTAACAATGATTGTCAATGTGACTCAAGCACTGTTTCT	50
OY	1224	gcattcgcgaattttccagaagaacagtg	1252
Db	49	CTACTTGGTATGTTTCCAGAAGATCGAG	21
RESULT	13		
LOCUS	BM408141	756 bp	mRNA linear EST 22-JAN-2002
DEFINITION	ESR582468 potato roots Solanum tuberosum cDNA clone CPR033GZ0 5'		
ACCESSION	BM408141		
VERSION	BM408141.1		
KEYWORDS	EST.		
SOURCE	potato.		
ORGANISM	Solanum tuberosum		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.		
AUTHORS	van der Hoeven,R., Sun,H., Karanycheva,S.A., Tsai,J., Van Aken,S., Uterback,T., Chienlingo,A., Bougri,O., Buell,C.R., Konning,C., Tanksley,S. and Baker,B.		
TITLE	Generation of ESTs from potato roots		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Research Genetics, Libraries Division Tel.: 1-800-711-6195 Email: cdna@resgen.com For clone info: Please contact Research Genetics, Libraries Division tel 1-800-711-6195, email cdna@resgen.com Seq primer: T3.		
FEATURES	Location/Qualifiers		
Source	1..756		
	/organism="Solanum tuberosum"		
	/cultivar="Kennebec"		
	/db_xref="taxon:4113"		
	/clone="CPR033GZ0"		
	/clone_lib="potato roots"		
	/tissue_type="roots"		
	/dev_stage="In vitro grown stem cuttings"		

/!ab=host="SOLR"  
/!ab=vector: pb1uescript SK(-); Site.1: ECoRI; Site.2:  
XhoI; supplier: Cornell University, Tanksley lab;  
sequencing: The Institute for Genomic Research. Roots were  
isolated from in vitro grown stem cuttings on CM medium.  
Roots were isolated two weeks after placing the stem  
cuttings from in vitro grown plants on medium."

Query Match	4.0%	Score 108.4	DB 10	Length 756
Best Local Similarity	52.72%	Pred. No. 1.1e-14		
Matches 235	Conservative 0	Mismatches 211	Indels 0	Gaps 0
BASE COUNT	229 a	150 c	166 g	211 t
ORIGIN				
OY	2261	aagctttccagaacacgcctcaagaagttgaagttggaagaacttactcaagctgtcat	2320	
DB	260	ATGCACCTTCCAGATCCTTAAGAGTTAACTTGAAGCTTCAACCTACCTGATGGGAGA	319	
OY	2321	acttggacatcatagctgaagttgctactgaagtgctgaagctgtagatgtagcgtt	2380	
DB	320	GTATGGCCCTCTCTTTGTATGATTACCGAATCTCGAGTACTCAACATAAGAAATTATGCC	379	
OY	2381	gttgggtggaagaatggatccaatgttataagttatgatgaagctttgtctaa	2440	
DB	380	TCACAGGTCACAAAGTGGGACAAAGTTGAAGAGGGGTTCCGTTCTTAAACATATGCTCA	439	
OY	2441	ttaatatagtttttccaaagttcgtgaaagccacaaatgacaacttctcgtctgagc	2500	
DB	440	TTGAGATATCTGATATTAATAACACTGGAGTGCCTCAATATGATATTTCTGTCTCGAAG	499	
OY	2501	gccctaatgattagaagttgcacaaattggaagaagataccattgagttgcagatatc	2560	
DB	500	ATCTGATCTCTTAAGAGTGTCTTCACTTGGACGACATCCCTCAGCATCGGAGATATTC	559	
OY	2561	acacacacagctgattgaagtaagaagtgctcccccacaaacttgaggatctgctgcac	2620	
DB	560	CGACTTTTGCAGATTAATTGAGCTGGAAATTTCAAGCCAATCTGCAGTGTCTTAAGCTAAG	619	
OY	2621	gaattcagaagaagaagaagacccctgcgaagaacaccttgtagtctglatctcaatc	2680	
DB	620	AGATCCAGAGGAGGACGACAAAGTATGGGTGAAGCAACTCAAGTGCAGATGAGAGAA	679	
OY	2681	catgaaaggagagtgatctctgattca	2706	
DB	680	ATTTCGGGAGATTAATATGCTGTTGCA	705	

RESULT 14	AM030063	417 bp	mRNA	linear	EST 18-MAY-2001
LOCUS	AM030063				
DEFINITION	EST273318	tomato callus,	TAMU Lycopersicon	esculentum	CDNA clone
ACCESSION	AM030063				
VERSION	AM030063.1	GI:5888819			
KEYWORDS	EST.				
SOURCE	tomato.				
ORGANISM	Lycopersicon	esculentum			
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
AUTHORS	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;				
	Asteridae; euasterids I; Solanales; Solanaceae; Solanum;				
	Lycopersicon.				
	1 (bases 1 to 417)				
	Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E.				
	, Liang,F., Upton,J., Craven,M.B., Bowman,C.L., Ahn,S., Roming,				
	,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.				
	Generation of ESTs from tomato callus tissue				
	Unpublished (1999)				
	Contact: CUGI				
	Clemson University Genomics Institute				
	Clemson University				
	100 Jordan Hall, Clemson, SC 29634, USA				
	Email: <a href="http://www.genome.clemson.edu/orders/index.html">http://www.genome.clemson.edu/orders/index.html</a>				





Thu Sep 12 15:30:10 2002

us-09-864-680-4.rst

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Page 11



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 11, 2002, 11:42:09 : Search time 881.41 Seconds  
(without alignments)  
6036.598 Million cell updates/sec

Title: US-09-864-680-2  
Perfect score: 3099  
Sequence: 1 caaatattcttgagtgaa.....tttagtttaaaaaaaaaa 3099

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: N.Geneseq\_032802.\*  
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3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.\*  
4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.\*  
5: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.\*  
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23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.\*  
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.\*  
25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the total score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3099	100.0	3099	22	AAD10204	Pepper Bs2 CDNA.
2	3099	100.0	3099	22	AA63302	Pepper Bs2 CDNA se
3	2725.6	88.0	31491	22	AAD10203	Pepper Bs2 gene.
4	2725.6	88.0	31491	22	AA63301	Pepper Bs2 resista
5	2718	87.7	2718	22	AA63303	Pepper Bs2 open re
6	272.8	8.8	2739	21	AA520262	Coding region of p
7	272.8	8.8	2817	21	AA520652	Coding region of p
8	272.8	8.8	3683	22	AA503713	DNA encoding Rx 25
9	272.8	8.8	10529	21	AA520264	Genomic DNA of pot

10	272.8	8.8	10329	21	AA520653	Genomic DNA encodi
11	271.8	8.7	5820	20	AA237153	DNA sequence of BA
12	269.6	8.6	3066	20	AA237154	Partial nucleotide
13	268	8.6	3014	22	AA503715	DNA encoding Rx 72
14	266.4	8.6	2880	22	AA503716	DNA encoding Rx 19
15	266	8.6	2885	22	AA503717	DNA encoding Rx 32
16	264.8	8.5	3283	22	AA503718	DNA encoding Rx 39
17	256.8	8.3	2679	22	AA503719	DNA encoding Rx 7,
18	172.2	5.6	5475	19	AAV17777	Tomato Prf CDNA.
19	170	5.5	10968	19	AAV17789	Tomato Prf genomic
20	149.2	4.8	3997	19	AAV26082	Tomato pest resist
21	149.2	4.8	9870	19	AAV13935	Tomato Mi resist
22	149.2	4.8	9870	19	AAV16457	Wild tomato Mi res
23	149.2	4.8	51952	19	AAV26083	Tomato pest resist
24	147.6	4.8	3982	19	AAV26084	Tomato pest resist
25	132.2	4.3	23670	24	ABA97077	Tomato Hero gene c
26	119	3.8	3909	24	ABA97078	Tomato Hero gene A
27	103.4	3.3	534	21	AA51884	N. tabacum Class I
28	95.2	3.1	540	21	AA51891	N. tabacum Class I
29	94.4	3.0	3801	21	AA559332	Nucleotide sequenc
30	94.4	3.0	6568	18	AA79882	Tomato immunity 2
31	92.2	3.0	532	21	AA51889	N. tabacum Class I
32	88.8	2.9	517	21	AA51884	N. tabacum Class I
33	83.6	2.7	4465	17	AA742135	I2C-2 gene encodin
34	81.4	2.6	477	21	AA51880	N. tabacum Enh4 ge
35	76	2.5	472	21	AA51876	N. tabacum Class I
36	74	2.4	644	21	AA51886	N. tabacum Class I
37	72.2	2.3	2862	21	AA58295	Sorghum resistance
38	70.4	2.3	647	21	AA51874	Rice disease resist
39	66.6	2.1	489	21	AA51874	N. tabacum Enh2 ge
40	62.8	2.0	1028	21	AA53996	Rice disease resist
41	59.2	1.9	2954	21	AA58294	Sorghum resistance
42	59.2	1.9	6760	21	AA58293	Sorghum resistance
43	56	1.8	4948	17	AA742134	I2C-1 gene encodin
44	50.4	1.6	5910	19	AA66798	Rice bacterial lea
45	48.2	1.6	548	21	AAA40001	Rice disease resist

## ALIGNMENTS

RESULT 1	
ID AAD10204	standard; cDNA; 3099 BP.
XX AAD10204:	
AC AAD10204:	
XX 24-SEP-2001 (first entry)	
DT 24-SEP-2001 (first entry)	
XX Pepper Bs2 CDNA.	
DE Pepper Bs2 CDNA.	
XX Bs2 gene; pepper; resistance gene; plant pathogen; virulence gene;	
KW bacterial spot disease; Xanthomonas campestris pv. vesicatoria;	
KW AVRBS2; hypersensitive response; transgenic plant; tomato; tobacco;	
KW rice; corn; wheat; ss.	
XX Capsicum annuum.	
OS Capsicum annuum.	
XX Key	Location/Qualifiers
FT CDS	93..2810
FT /tag- a	
FT /product- "Bs2 protein"	
FT /note- "this region is claimed as SEQ ID NO:4	
FT In claim 7"	
XX US6262343-B1.	
PN 17-JUL-2001.	
XX 23-JUL-1999.	99US-0360186.
PF 23-JUL-1998.	98US-0093957.
XX	



Db 1561 acattttatcatgaacagacatgttcttgacgtatcatatccagaatgtcatatctc 1620  
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 Db 1621 gtatgtataaagcagcccttaagcggtgagctgtgtatgaataatattatgtccct 1680  
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 Db 1801 ttctcaatcagaaggtgtgttcttcaatctcaaatccttgagccttgagacagac 1860  
 QY 1861 agatgtatgtttccctcagagataactaagcctcatctgttgaggtactatcatgt 1920  
 Db 1861 agatgtatgtttccctcagagataactaagcctcatctgttgaggtactatcatgt 1920  
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 Db 1921 tcaagctatgggaatttcgaatgtacccctcagaatcttgcaagttatggaaatcagaat 1980  
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 Db 3001 attcaactcaagtaactagcagaccacacatggttgattgtgagttgattgattatt 3060  
 QY 3061 tatacgaatgagacacacagtttatttataaaaaaaa 3099  
 Db 3061 tatacgaatgagacacacagtttatttataaaaaaaa 3099

RESULT 2  
 AAF63302  
 ID AAF63302 standard; cDNA; 3099 BP.  
 AC AAF63302;  
 XX  
 DT 02-MAY-2001 (first entry)  
 DE  
 DE Pepper Bs2 cDNA sequence.  
 XX  
 XX Bs2; pepper; pathogen resistant; Xanthomonas campestris pv vesicatoria;  
 KW Xcv; bacterial spot disease; transgenic plant; crop; fruit; flower; ss.  
 XX  
 OS Capsicum annuum.  
 XX  
 PN WO200107635-A1.  
 XX  
 PD 01-FEB-2001.  
 XX  
 PF 23-DEC-1999; 99WO-US30891.  
 XX  
 PR 23-JUL-1999; 99US-0360186.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Straskawicz BJ, Dahlbeck D, Tai TH;  
 XX  
 DR WPI: 2001-168560/17.  
 XX  
 DR P-PSDB; AAB72198.  
 PT Novel Bs2 polypeptide from Capsicum annuum for producing transgenic  
 PT plants having resistance to bacterial spot disease caused by  
 PT Xanthomonas campestris pv vesicatoria (Xcv) -  
 XX  
 PS Claim 3; Page 57-61; 72pp; English.  
 XX  
 CC This invention relates to the amino acid sequence of the Bs2 protein  
 CC isolated from Capsicum annuum (pepper). The protein and DNA sequences of  
 CC Bs2 can be used to confer resistance to the plant pathogen Xanthomonas  
 CC campestris pv vesicatoria (Xcv) which causes bacterial spot disease. Bs2  
 CC DNA and protein sequences are useful for producing transgenic plants such  
 CC as pepper, tomato, tobacco, broccoli, cauliflower, cabbage, canola,  
 CC cowpea, grape, bean soybean, rice, corn, wheat, barley, citrus, cotton,

CC cassava and walnut, having resistance to *X. campestris*. The protein and  
 CC DNA molecule are also useful for producing transgenic alfalfa, flax,  
 CC sunflower, safflower, brassica, peanut, clover, lettuce, cucurbits,  
 CC potato, carrot, radish, pea, lentils, apples, pears, peaches, apricots,  
 CC carnations and roses having resistance to *X. campestris*. The present  
 CC sequence represents cDNA encoding Bs2.

XX Sequence 3099 BP; 970 A; 514 C; 693 G; 922 T; 0 other;

Query Match 100.0%; Score 3099; DB 22; Length 3099;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3099; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 61 tcgcaaaagacaaaacagaaatacagatataatgctcatgcaagtggtgtctctta 120  
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 Db 301 ttgcaagtcgtctgaataacacatctcaactcgaactgaacgaacgaacttacttggaagaa 360  
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Db	2041	tgcacatlaagggacacttcaaacctgcgccagaatttattttgcagatttggccaaagtcatg	2100
QY	2101	ttggcagaaggaaggcacttggatttttccaaacttacaactatttcttaacttgcctcac	2160
Db	2101	ttggcagaaggaaggcacttggatttttccaaacttacaactatttcttaacttgcctcac	2160
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QY	2221	gaataaagatgactataaaagtttctcgggactctgggtctccacaacactctgtctac	2280
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QY	2461	tgggtgagcgtctatttgggtggagaagaatggcaccacaatttctatggagtttaacgatga	2520
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QY	2581	ctgtgccttgggcgcctccatgattatagaagtttgcanaaatttgaagaagatgaccattagtt	2640
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QY	2641	ttgcagatatatacacacactacagctgattgagttgaagagtggtcctccaaacttgggg	2700
Db	2641	ttgcagatatatacacacactacagctgattgagttgaagagtggtcctccaaacttgggg	2700
QY	2701	aatttgtgtgcagaatttccgaagaagaagaagacctcgggaacacacctgtgtgatttc	2760
Db	2701	aatttgtgtgcagaatttccgaagaagaagaagacctcgggaacacacctgtgtgatttc	2760
QY	2761	gtacctcaaaatccatctgaaggaagagtgatctcgatctgcagaagaacatttagaagaagctc	2820
Db	2761	gtacctcaaaatccatctgaaggaagagtgatctcgatctgcagaagaacatttagaagaagctc	2820
QY	2821	caagggccagaagaagatggaactcttgggatttcaatttcggccctcatcaaaaaataccac	2880
Db	2821	caagggccagaagaagatggaactcttgggatttcaatttcggccctcatcaaaaaataccac	2880
QY	2881	taaatatctcggcttccaagaacatgtggaattccaaaggagatgtgataccttttgttgt	2940
Db	2881	taaatatctcggcttccaagaacatgtggaattccaaaggagatgtgataccttttgttgt	2940
QY	2941	aaacatacttttgagtgtgaactgattccctctccctccctctttaaqtgaacttacta	3000
Db	2941	aaacatacttttgagtgtgaactgattccctctccctccctctttaaqtgaacttacta	3000
QY	3001	attcaaatcaagttactgaagacagacacaggttggatttggatcgaggttggattgaattc	3060
Db	3001	attcaaatcaagttactgaagacacagacaggttggatttggatcgaggttggattgaattc	3060
QY	3061	tatacgtatgagacacaccagtttagttttaaaaaaaaaa 3099	

Db	3061	tatacgtatgagacaaccagtttgatttcaaaaaaaaaa	3099
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RESULT	3		
ID	AD10203		
AC	AD10203 standard; DNA; 31491 BP.		
XX	AD10203;		
DT	24-SEP-2001 (first entry)		
DE	Pepper Bs2 gene.		
XX			
KM	Bs2 gene; pepper; resistance gene; plant pathogen; virulence gene;		
KW	bacterial spot disease; Xanthomonas campestris pv. vesicatoria;		
AV	Abs2; hypersensitive response; transgenic plant; tomato; tobacco;		
Rice	rice; corn; wheat; ds.		
OS	Capsicum annuum.		
XX			
FH	Key	Location/Qualifiers	
FT	promoter	1..502	
FT		/tag= a	
FT	exon	503..554	
FT		/tag= b	
FT		/number=1	
FT	Intron	/note="this region contains a portion of 5' untranslated region (5' UTR)"	
FT		555..1439	
FT		/tag= c	
FT		/number=1	
FT	exon	/note="the 5' untranslated region (5' UTR) continues in this region"	
FT		1440..4162	
FT		/tag= d	
FT		/number=2	
FT	CDS	/note="The region 1440-1479 contains 5' UTR which is followed by the coding region"	
FT		1480..31219	
FT		/tag= e	
FT	Intron	/product= "Bs2 protein" 4163..31184	
FT		/tag= f	
FT	exon	/number=2 31185..31216	
FT		/tag= g	
FT		/number=3 31220..31491	
FT	3'UTR	/tag= h	
XX			
PN	US6262343-B1.		
XX			
DD	17-JUL-2001.		
PP	23-JUL-1999;	99US-0360186.	
PR	23-JUL-1998;	98US-0093957.	
PA	(REGC ) UNIV CALIFORNIA.		
PI	Staskiewicz BJ, Dahlbeck D, Tai TH;		
DR	WPJ; 2001-450496/48.		
DR	P-Psdb; AAE05409.		
XX			
XX	Nucleic acid molecules encoding Bs2 protein, useful for producing transgenic plants having resistance to the plant pathogen Xanthomonas campestris -		
Claim	7, Column 21-50; 37pp; English.		
The	present sequence is Bs2 gene from pepper. The Bs2 gene is shown		

to confer resistance to plant pathogen *Xanthomonas campestris* pv. *vesicatoria* which causes bacterial spot disease. The Bs2 protein has Bs2 biological activity, i.e., when co-expressed in a plant with a *X. campestris* AvrBs2 gene product, it produces a localised hypersensitive response. The protein includes a nucleotide binding motif and leucine rich repeats of the type found in other plant resistance genes. The Bs2 nucleic acid molecule is useful for producing transgenic plants such as pepper, tomato, tobacco, broccoli, cauliflower, cabbage, cowpea, grape, canola, bean, soybean, rice, corn, wheat, barley, citrus, cotton, cassava and walnut, that are resistant to plant pathogen *Xanthomonas campestris*. The transgenic plants produced using Bs2 molecule develop a hypersensitive response to the pathogen at the site of inoculation and show an enhanced resistance to systemic infection. The Bs2 nucleic acid molecule is also useful as polymerase chain reaction (PCR) primers for amplifying portions of Bs2 nucleic acid molecule, as sequencing primers to verify the authenticity of an amplified molecule, and as hybridisation probes.

Query Match	88.0%;	Score 2725.6;	DB 22;	Length 31491;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 2728; Conservative	0;	Mismatches	4;	Indels 0; Gaps 0;

OY	53	ggtatattgtcgcaaaagacaaanaacgagatcatcgatataatagtgtctctgtgaagtgtggc	112
Db	1440	ggctaatatgtcgcaaaagacaaanaacgagatcatcgatataatagtgtctctgtgaagtgtggc	1499
OY	113	tctctctatagaaacaataagaaatctctctctgtgcatctcaattctgcgcgaatgtcatctatc	172
Db	1500	tctctctatagaaacaataagaaatctctctctgtgcatctcaattctgcgcgaatgtcatctatc	1559
OY	173	ctgtgtatccaagagaaagaactttgcgcctctctgtgaaaaagttaattccctcggaaagtattc	232
Db	1560	ctgtgtatccaagagaaagaagaactttgcgcctctctgtgaaaaagttaattccctcggaaagtattc	1619
OY	233	tgctcaagaaccttvgagaaacaacatgttttttggggaaatvgaaaggttttcttgaagttagagt	292
Db	1620	tgctcaagaaccttvgagaaacaacatgttttttggggaaatvgaaaggttttcttgaagttagagt	1679
OY	293	aagsgaaagtvtgcaagvtgcgtctgtaatatcaacaatctcaactagaaactaagaagaactgtact	352
Db	1660	aagsgaaagtvtgcaagvtgcgtctgtaatatcaacaatctcaactagaaactaagaagaactgtact	1739
OY	353	ggggagaaataataaagcccaagaaaaaaaaggccgcgtcgaagaagtttctgtcaaaagccctgcaca	412
Db	1740	ggggagaaataataaagcccaagaaaaaaaaggccgcgtcgaagaagtttctgtcaaaagccctgcaca	1799
OY	413	agtagcagagagacatgtgatatatactctggaaagagtcgcgaagaagatccacaagataaagysaa	472
Db	1800	agtagcagagagacatgtgatatatactctggaaagagtcgcgaagaagatccacaagataaagysaa	1859
OY	473	acaaagtctcaaaaggaatcatgttgtatatttttcaaaagtttcaaaatcaaaaacgatatittgaa	532
Db	1860	acaaagtctcaaaaggaatcatgttgtatatttttcaaaagtttcaaaatcaaaaacgatatittgaa	1919
OY	533	ggttaagaacacataatgttttggacgtgtatcatcaaaagaaacagttgtttagaagaatctgcac	592
Db	1920	ggttaagaacacataatgttttggacgtgtatcatcaaaagaaacagttgtttagaagaatctgcac	1979
OY	593	tagaaagtactacttvgggaaaccccaaaatctaccgatgttcggagatvgggagatagtgtaa	652
Db	1980	tagaaagtactacttvgggaaaccccaaaatctaccgatgttcggagatvgggagatagtgtaa	2039
OY	653	aacaaccttagcaaaagaagttttaacaatgtatgaatcaatctcatgtcggtttttagatgttca	712
Db	2040	aacaaccttagcaaaagaagttttaacaatgtatgaatcaatctcatgtcggtttttagatgttca	2099
OY	713	tgacctggggtctacatatactcaacagacacaacaaaagaaatttgcgtgggccttctgcga	772
Db	2100	tgacctggggtctacatatactcaacagacacaacaaaagaaatttgcgtgggccttctgcga	2159

QY	773	ttccaacatcaaaatgatacagaggtttaagatgatttggatgaagcagagctcagacacat	832
Db	2160	ttccaacatcaaaatgatacagaggtttaagatgatttggatgaagcagagctcagacacat	2219
QY	833	gttccagaaaaggtttaagaggaagaggttaacttaatttgcctctgatacctcagatg	892
Db	2220	gttccagaaaaggtttaagaggaagaggttaacttaatttgcctctgatacctcagatg	2279
QY	893	tgaagtctggatgagcgctgagacgatactcttccaactgaaagaacatgcagagagtcgaat	952
Db	2280	tgaagtctggatgagcgctgagacgatactcttccaactgaaagaacatgcagagagtcgaat	2339
QY	953	actcttgaactacccggtaataagataagttaaactctgttaatctgttgatgagaaattctctc	1012
Db	2340	actcttgaactacccggtaataagataagttaaactctgttaatctgttgatgagaaattctctc	2399
QY	1013	gcgagatgagcttcaatgatacaagaatgaagatttggagctcttccaagaatgcagacatttc	1072
Db	2400	gcgagatgagcttcaatgatacaagaatgaagatttggagctcttccaagaatgcagacatttc	2459
QY	1073	aagtgaaagcattaccataatgaatctgaagctgtttgaaagagcaatcggagagtgaaatga	1132
Db	2460	aagtgaaagcattaccataatgaatctgaagctgtttgaaagagcaatcggagagtgaaatga	2519
QY	1133	cgggtttacccaattacatacttctcgctgtccagaggtcttccaacttcaaaagagacaataga	1192
Db	2520	cgggtttacccaattacatacttctcgctgtccagaggtcttccaacttcaaaagagacaataga	2579
QY	1193	agatttgagaacactgtctgtcctaagaatgatacgaatcctgcgtcacaaatgatacctgataagc	1252
Db	2580	agatttgagaacactgtctgtcctaagaatgatacgaatcctgcgtcacaaatgatacctgataagc	2639
QY	1253	atgttccaagctgtgtcttgggttgcgtgaattacgaatacctctgaaacagcgaatccaacaaactgct	1312
Db	2640	atgttccaagctgtgtcttgggttgcgtgaattacgaatacctctgaaacagcgaatccaacaaactgct	2699
QY	1313	tcctgcatctcggaaatttttccaagaagaacagtgataatctccagtgaagaaattctgatagagatc	1372
Db	2700	tcctgcatctcggaaatttttccaagaagaacagtgataatctccagtgaagaaattctgatagagatc	2759
QY	1373	atggaatgagcttgagaggggttccttgaaagtcttgaaaaatgaatttgagaagagaggtcttgaaagt	1432
Db	2760	atggaatgagcttgagaggggttccttgaaagtcttgaaaaatgaatttgagaagagaggtcttgaaagt	2819
QY	1433	tttgaaagaagctcttgcataatagatgcagtcctccgcgcagacaagaagaatctgagaatggac	1492
Db	2820	tttgaaagaagctcttgcataatagatgcagtcctccgcgcagacaagaagaatctgagaatggac	2879
QY	1493	aaaaatagatcatgataaggttcaatgatactataataatgacccgtgcgtggaagaagaatttca	1552
Db	2880	aaaaatagatcatgataaggttcaatgatactataataatgacccgtgcgtggaagaagaatttca	2939
QY	1553	aagggagaacatttttcaatgaaacagacattgtctcttgacgtatcatataccaagaatgtctc	1612
Db	2940	aagggagaacatttttcaatgaaacagacattgtctcttgacgtatcatataccaagaatgtctc	2999
QY	1613	atatctctgatatgataaataatgcagccctttaaagcgcgtgacatgataatgaataatata	1672
Db	3000	atatctctgatatgataaataatgcagccctttaaagcgcgtgacatgataatgaataatata	3059
QY	1673	ttgtcccatatgattttaaagagctcttcttaccctctgaaatctgaaatctgaaagatca	1732
Db	3060	ttgtcccatatgattttaaagagctcttcttaccctctgaaatctgaaatctgaaagatca	3119
QY	1733	tgaacaacaacatcttcttgaaacgaacccaattgttttcttcttcaactcttgagccctt	1792
Db	3120	tgaacaacaacatcttcttgaaacgaacccaattgttttcttcttcaactcttgagccctt	3179
QY	1793	ataattaatcttccaatcagaaggtgttgaattccaataatcactccaagaagctctggagcgcgag	1852
Db	3180	ataattaatcttccaatcagaaggtgttgaattccaataatcactccaagaagctctggagcgcgag	3239



QY	1853	acacagacagaatctgatagtttccctcgagagatacctaagcccaactcgtgttgagttacct	1912
Db	3240	acacagacagaatctgatagtttccctcgagagatacctaagcccaactcgtgttgagttacct	3299
QY	1913	atcatctgttcagctatgaggaatttcgatgtacccccaagaatttcaggtttatgtacct	1972
Db	3300	atcatctgttcagctatgaggaatttcgatgtacccccaagaatttcaggtttatgtacct	3359
QY	1973	gcacaattcattgtctcaacggtttctgaatcagataataaattttgtctgaggaatttg	2032
Db	3360	gcagacattcattgtctcaacggtttctgaatcagataataaattttgtctgaggaatttg	3419
QY	2033	ggaactaatgcgaataaagagcgaactcttaactcgcgcagattttattttggccaagttgccaa	2092
Db	3420	ggaactaatgcgaataaagagcgaactcttaactcgcgcagattttattttggccaagttgccaa	3479
QY	2093	tggatctctttacaaaggaaggcactcttgattttccaactaccacaactatttctacct	2152
Db	3480	tggatctctttacaaaggaaggcactcttgattttccaactaccacaactatttctacct	3539
QY	2153	gtctccacggttgctgacagaaaggaggttatattatgggagttccagaatgtcaaaaaataag	2212
Db	3540	gtctccacggttgctgacagaaaggaggttatattatgggagttccagaatgtcaaaaaataag	3599
QY	2213	aatcagttggaataaagatgagactataaagaatttcgagacctcggtgtccccaacatct	2272
Db	3600	aatcagttggaataaagatgagactataaagaatttcgagacctcggtgtccccaacatct	3659
QY	2273	tgtctactctgcagcaacttgtaaatatgtagtcttatatctgtttgatattagacctttgctc	2332
Db	3660	tgtctactctgcagcaacttgtaaatatgtagtcttatatctgtttgatattagacctttgctc	3719
QY	2333	agtgtatcattccaagtgagcaaaagcctttccagcaagcgtccaaagaagtgaagttggaag	2392
Db	3720	agtgtatcattccaagtgagcaaaagcctttccagcaagcgtccaaagaagtgaagttggaag	3779
QY	2393	aactatctaaagctggttcaacttggacatcatagctgagttgctctaaaccttgagttgct	2452
Db	3780	aactatctaaagctggttcaacttggacatcatagctgagttgctctaaaccttgagttgct	3839
QY	2453	gaagctgagtgatgagagcgttgtttgttgaagaatgcatccaatgtgtatgggatttaa	2512
Db	3840	gaagctgagtgatgagagcgttgtttgttgaagaatgcatccaatgtgtatgggatttaa	3899
QY	2513	tcgatctgaagccttttgcataataatagttttctcgaagttcttggaagccacaataga	2572
Db	3900	tcgatctgaagccttttgcataataatagttttctcgaagttcttggaagccacaataga	3959
QY	2573	caattttctgtcccttgagagcgctctatgatatgaagttgaaaaaatttgaagaagatacc	2632
Db	3960	caattttctgtcccttgagagcgctctatgatatgaagttgaaaaaatttgaagaagatacc	4019
QY	2633	catctgagtttcagatatatacacacactacacagctgagttgaagagagttgctcccaa	2692
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QY	2693	acttgggggaactcgtcgtcagcgaatttcgaaagaacaagaagacctcgaaacaacccgtg	2752
Db	4080	acttgggggaactcgtcgtcagcgaatttcgaaagaacaagaagacctcgaaacaacccgtg	4139
QY	2753	ggatgttcgcatctccaatccatctgaagagga	2784
Db	4140	ggatgttcgcatctccaatccatctgaagagga	4171
RESULT	4		
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XX	AAF63301	standard; DNA; 31491 BP.	
XX	AAF63301;		
XX	02-MAY-2001	(first entry)	

Query Match	Best Local Similarity	88.0%;	Score 2725.6;	DB 22;	Length 31491;	
Matches 2728;	Conservative	99.9%;	Pred. No. 0;	Mismatches 4;	Indels 0;	Gaps 0;
QY 53	ggtcatagtgtgcgaagagacaaaaacgagataacagtatatatggtcctatgtaagttgtgc	112				
DB 1440	ggtcatagtgtgcgaagagacaaaaacgagataacagtatatatggtcctatgtaagttgtgc	1499				
QY 113	ttctctatgagaacaatagatctctcttgcattcattcgccgattgcatctctatc	172				
DB 1500	ttctctatgagaacaatagatctctcttgcattcattcgccgattgcatctctatc	1559				
QY 173	ctgtgattcacaaggaagaacttgcgtctcttctgtgaaaaagttaagttccctgtgaagttatt	232				
DB 1560	ctgtgattcacaaggaagaacttgcgtctctctgtgtgaaaaagttaagttccctgtgaagttatt	1619				
QY 233	tgctcaagaactttgagaaaaacaatglttttggggaaatgaaagatttgaagtgaagtt	292				
DB 1620	tgctcaagaactttgagaaaaacaatglttttggggaaatgaaagatttgaagtgaagtt	1679				
QY 293	aagagaagtttgcaagtgtctgtgaatcacaaattcaacttgaagctaacaggaacttact	352				
DB 1680	aagagaagtttgcaagtgtctgtgaatcacaaattcaacttgaagctaacaggaacttact	1739				
QY 353	gggagaataataaaagccagaaaaaaagcgctgcgaagtttcgtltaaaagcctgcacaa	412				
DB 1740	gggagaataataaaagccagaaaaaaagcgctgcgaagtttcgtltaaaagcctgcacaa	1799				

QY 413 agtaagacagagcatgatacatatctggaagaagtcgacaagaatccacaagaataagagaa 472  
|||||  
Db 1800 agtaacagagagacatgatacatatctggaagaagtcgacaagaatccacaagaataagagaa 1859  
QY 473 acaagatcaagaagatattggtttcattgatttttcaagttccacaagaatatttgaa 532  
|||||  
Db 1860 acaagatcaagaagatattggtttcattgatttttcaagttccacaagaatatttgaa 1919  
QY 533 ggttaagaacaatagttgtagcgtgtagatcaagaagaacagttgttagaagaatctgac 592  
|||||  
Db 1920 ggttaagaacaatagttgtagcgtgtagatcaagaagaacagttgttagaagaatctgac 1979  
QY 593 tagaaggtcattctggtggagaccccaagtlcatcccgattgtcggaatgggaagcagtagaa 652  
Db 1980 tagaaggtcattctggtggagaccccaagtlcatcccgattgtcggaatgggaagcagtagaa 2039  
QY 653 aacaacctagcaaaagaagtttcaatgatgatgaatcattctatgcccgttttgatgtca 712  
|||||  
Db 2040 aacaacctagcaaaagaagtttcaatgatgatgaatcattctatgcccgttttgatgtca 2099  
QY 713 tgccttggtctacatctcatcacagcaacaacaaagaatattgtctggcctctgca 772  
|||||  
Db 2100 tgccttggtctacatctcatcacagcaacaacaaagaatattgtctggcctctgca 2159  
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QY 833 gtacacagaaagtttaagaagaagaggttaattatgttcttgatgatatctcggaattg 892  
Db 2220 gtacacagaaagtttaagaagaagaggttaattatgttcttgatgatatctcggaattg 2279  
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Db 2280 tgaagtgtaggaatggtgtagacagatgcttccaactgaagaacatgacagagagtcogaa 2339  
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QY 1073 aagttgaagcatctaccatagatgttcgaagctgttggaaagcaaatccgagatgaatgtca 1132  
Db 2460 aagttgaagcatctaccatagatgttcgaagctgttggaaagcaaatccgagatgaatgtca 2519  
QY 1133 cgggttaaccaactattgtctgttgcgttcgaaggtcttccaacttaaaagaacataaga 1192  
Db 2520 cgggttaaccaactattgtctgttgcgttcgaaggtcttccaacttaaaagaacataaga 2579  
QY 1193 agattggaacaaactgttgcataaagatgtcaagtcattcgtcacaaatgatacctgtagaag 1252  
Db 2580 agattggaacaaactgttgcataaagatgtcaagtcattcgtcacaaatgatacctgtagaag 2639  
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Db 2640 atgttaacgtgtgctgtggtttgaatgaatcatttgaacaaagcagatctaaacatgtct 2699  
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QY 1373 atggaatggtctgaggggtcttcctgaagttggaataatggaagagaggttgaagaatgt 1432  
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QY 1433 ttggaagagctgtgcgataagatgtcgtagctcgttcgaagagaaatgtagatggagac 1492  
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QY 1493 aaaaattagatcatgtgaagttcatgataatataatgacctgtgtgagagaagatgtca 1552

Db 2880 aaaaattagatcatgtgaagttcatgataatcaatataatgacctgtgtgagagaatgtca 2939  
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QY 1613 atattctgtatgtataaataatgagcccttgaagcgtgtgactgtgtgataatgaatga 1672  
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Db 3060 ttgtccctatggtccttataagaggtcttcttaacccctgtaaatctgcaatgtgaagatca 3119  
QY 1733 tgaacaacaacatcttgaacacgaaccccatctgttctctcttctcatctctgaacctt 1792  
Db 3120 tgaacaacaacatcttgaacacgaaccccatctgttctctcttctcatctctgaacctt 3179  
QY 1793 atattatgttctcaaatcagaggtgtgttattcaattcaattcaaatcctgagagctgag 1852  
Db 3180 atattatgttctcaaatcagaggtgtgttattcaattcaaatcctgagagctgag 3239  
QY 1853 acaacagacagattgtagtcttccctcgagagatactaaagcccatctgttgaagttact 1912  
Db 3240 acaacagacagattgtagtcttccctcgagagatactaaagcccatctgttgaagttact 3299  
QY 1913 atcaattgttcagctatgggaatttcogaltgatacctccagaanaattgcaagttatggaatct 1972  
Db 3300 atcaattgttcagctatgggaatttcogaltgatacctccagaanaattgcaagttatggaatct 3359  
QY 1973 gcagacatcatgttctcaacggttccogattcogataataatattttgttgtaggaattgt 2032  
Db 3360 gcagacatcatgttctcaacggttccogattcogataataatattttgttgtaggaattgt 3419  
QY 2033 ggaactaatgcaatlaaagagcatctaaactgcccagatcttattatgccaagtctcccaag 2092  
Db 3420 ggaactaatgcaatlaaagagcatctaaactgcccagatcttattatgccaagtctcccaag 3479  
QY 2093 tggattcttgaacaaagaagagccattgatttttccaactcaacataatttctact 2152  
Db 3480 tggattcttgaacaaagaagagccattgatttttccaactcaacataatttctact 3539  
QY 2153 gttccacgttctgttcacgaagagaggttatatagtggaattcagaatgtccaacaaatcag 2212  
Db 3540 gttccacgttctgttcacgaagagaggttatatagtggaattcagaatgtccaacaaatcag 3599  
QY 2213 aatcagtggaataaagagtagactataaagtttccggagctctgggtctcccaaatct 2272  
Db 3600 aatcagtggaataaagagtagactataaagtttccggagctctgggtctcccaaatct 3659  
QY 2273 tgtcatctgagcaaaccttgaataatgaggtctatatactggttgaatagccctttgccc 2332  
Db 3660 tgtcatctgagcaaaccttgaataatgaggtctatatactggttgaatagccctttgccc 3719  
QY 2333 agtgatcaattccaagtccaagaagcttctccagcaacgctccaagaagttggaagttggaag 2392  
Db 3720 agtgatcaattccaagtccaagaagcttctccagcaacgctccaagaagttggaagttggaag 3779  
QY 2393 aactatcatagctgtgtcatatacttgagacatcatagctgaggttgcctaaacctgaagtgct 2452  
Db 3780 aactatcatagctgtgtgtcatatacttgagacatcatagctgaggttgcctaaacctgaagtgct 3839  
QY 2453 gaaactgaatgatacgcctgtgtgtgtagaagaatgtagcacaactgttattgtgaatttaa 2512  
Db 3840 gaaactgaatgatacgcctgtgtgtgtgtagaagaatgtagcacaactgttattgtgaatttaa 3899  
QY 2513 tgcattgaagccttctgtcaataatagtttctccaaagttctggaagccacaataga 2572  
Db 3900 tgcattgaagccttctgtcaataatagtttctccaaagttctggaagccacaataga 3959  
QY 2573 caatttccgtctctgagagcctcagtgatgaagttgcaaaatctgaaagagatcac 2632  
|||||

Db 3960 caatttcctctccttgagcgcctcatgtattagaaattgcacaaatttgaagaagatacc 4019  
Qy 2633 cattgaatttgagatatacacacactacagctgattgagaaagatgtctctccaa 2692  
Db 4020 cattgaatttgagatatacacacactacagctgattgagaaagatgtctctccaa 4079  
Qy 2693 acttgggggaattctgtctgcagaaattcagaagaagaagacctctggaaacacctgt 2752  
Db 4080 acttgggggaattctgtctgcagaaattcagaagaagaagacctctggaaacacctgt 4139  
Qy 2753 ggaatttgcattcctcaatccattgaaagaga 2784  
Db 4140 ggaatttgcattcctcaatccattgaaagaga 4171

RESULT 5  
AAF63303  
ID AAF63303 standard; cDNA; 2718 BP.  
XX  
AC AAF63303;  
XX  
DT 02-MAY-2001 (first entry)  
XX  
DE Pepper Bs2 open reading frame sequence.  
XX  
KM Bs2; pepper; pathogen resistant; Xanthomonas campestris pv vesicatoria;  
KM Xcv; bacterial spot disease; transgenic plant; crop; fruit; flower; ss.  
OS Capsicum annuum.  
XX  
PN WO200107635-A1.  
XX  
PD 01-FEB-2001.  
XX  
PF 23-DEC-1999; 99WO-US30891.  
XX  
PR 23-JUL-1999; 99US-0360186.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Staskawicz BJ, Dahlbeck D, Tai TH;  
XX  
DR WPI: 2001-168560/17.  
DR P-PSDB; AAB72198.  
XX  
XX Novel Bs2, polypeptide from Capsicum annuum for producing transgenic  
PT plants having resistance to bacterial spot disease caused by  
PT Xanthomonas campestris pv vesicatoria (Xcv) -  
PS Claim 3; Page 64-68; 72pp; English.  
XX  
XX This invention relates to the amino acid sequence of the Bs2 protein  
CC isolated from Capsicum annuum (pepper). The protein and DNA sequences of  
CC Bs2 can be used to confer resistance to the plant pathogen Xanthomonas  
CC campestris pv vesicatoria (Xcv) which causes bacterial spot disease. Bs2  
CC DNA and protein sequences are useful for producing transgenic plants such  
CC as pepper, tomato, tobacco, broccoli, cauliflower, cabbage, canola,  
CC cowpea, grape, bean soybean, rice, corn, wheat, barley, citrus, cotton,  
CC cassava and walnut, having resistance to X. campestris. The protein and  
CC DNA molecule are also useful for producing transgenic alfalfa, flax,  
CC sunflower, safflower, brassica, peanut, clover, lettuce, cucurbits,  
CC potato, carrot, radish, pea, lentils, apples, pears, peaches, apricots,  
CC carnations and roses having resistance to X. campestris. The present  
CC sequence represents the open reading frame of Bs2.  
XX  
SQ Sequence 2718 BP; 851 A; 454 C; 623 G; 790 T; 0 other;

Query Match 87.7%; Score 2718; DB 22; Length 2718;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2718; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 atggtccatgcaagtggtgtctctcttatgagaacaatagaatctctctgacatcaat 152

Db 1 atggtccatgcaagtggtgtctctcttatgagaacaatagaatctctctgacatcaat 60  
Qy 153 tcgcgatgcaatctctatctctgtatcaacagagaagaacttgcgtctctgtgaaaaa 212  
Db 61 tcgcgatgcaatctctatctctgtatcaacagagaagaacttgcgtctctgtgaaaaa 120  
Qy 213 gttatgtccctgtgaagtatttgcagaagaacttggagaaaaaacatgtttttgggaatg 272  
Db 121 gttatgtccctgtgaagtatttgcagaagaacttggagaaaaaacatgtttttgggaatg 180  
Qy 273 acggaatttgaagtagagtagaagaagtgtcgaagtgtcgtcaatatacacaaattcactg 332  
Db 181 acggaatttgaagtagaagaagtgtcgaagtgtcgtcaatatacacaaattcactg 240  
Qy 333 agactacaggaactgtactgtggagaaaaataaaagccagaaaaaaaagcgctcgaaag 392  
Db 241 agactacaggaactgtactgtggagaaaaataaaagccagaaaaaaaagcgctcgaaag 300  
Qy 393 ttctgtcaaaagcctgcgaacaagtagcagaagacatggaatcctgtgaaagagtgaca 452  
Db 301 ttctgtcaaaagcctgcgaacaagtagcagaagacatggaatcctgtgaaagagtgaca 360  
Qy 453 aagatccagaataaggaacaaacagatatacaaaaggaatcattgttcaatatttcaagt 512  
Db 361 aagatccagaataaggaacaaacagatatacaaaaggaatcattgttcaatatttcaagt 420  
Qy 513 tcaacaaacagatatttgaaggttaagaacaataatgttgaagtgatgtatcaagaagaa 572  
Db 421 tcaacaaacagatatttgaaggttaagaacaataatgttgaagtgatgtatcaagaagaa 480  
Qy 573 cagtttttagaagatcgtacatgaagctactctgtgggaacccaagatcccgatgttc 632  
Db 481 cagtttttagaagatcgtacatgaagctactctgtgggaacccaagatcccgatgttc 540  
Qy 633 gggatgggaagcattgaaacaaacacttgcagaagaagttaacaatgtatgaatcaat 692  
Db 541 gggatgggaagcattgaaacaaacacttgcagaagaagttaacaatgtatgaatcaat 600  
Qy 693 ctatgccgttttgaatgtatcctgtgtgctacatatacacaagcacaacaaagaagaa 752  
Db 601 ctatgccgttttgaatgtatcctgtgtgctacatatacacaagcacaacaaagaagaa 660  
Qy 753 atttgcgtgcttccgtgcattccacaataaaattgaatgaaggttaagatgtatgt 812  
Db 661 atttgcgtgcttccgtgcattccacaataaaattgaatgaaggttaagatgtatgt 720  
Qy 813 gaaagcagctagcagacatgtttacagaagaagttaagaagaagagactaattgttc 872  
Db 721 gaaagcagctagcagacatgtttacagaagaagttaagaagaagagactaattgttc 780  
Qy 873 ttgatgatatctggaagtgtgaagtggtgagtggtgagcagatgtcttccaactgaa 932  
Db 781 ttgatgatatctggaagtgtgaagtggtgagtggtgagcagatgtcttccaactgaa 840  
Qy 933 gaaatgcaaggggtgcaatctgttgaatcccgtaatatgaagtagctgtgaaact 992  
Db 841 gaaatgcaaggggtgcaatctgttgaatcccgtaatatgaagtagctgtgaaact 900  
Qy 993 ggttgaagaattttcttgcgagatagcttcaatgataagaatgtggaagttc 1052  
Db 901 ggttgaagaattttcttgcgagatagcttcaatgataagaatgtggaagttc 960  
Qy 1053 ttcaaaagtgcaagcatttcaagtgaagcattaccatagatgttcgagactgttgaag 1112  
Db 961 ttcaaaagtgcaagcatttcaagtgaagcattaccatagatgttcgagactgttgaag 1020  
Qy 1113 caaatgcaagatgaatgaacgggtttacccaatttctgtggttgcagggctctc 1172  
Db 1021 caaatgcaagatgaatgaacgggtttacccaatttctgtggttgcagggctctc 1080  
Qy 1173 aaatctaaggaacatagaagattggaagaactgttctaagaatgtcgaatgtatcgtc 1232

Db	1081	aaacttaaaagacataatagaaggttggaaaaactggttcctaaagatgtaagtcattgctc	1140
OY	1233	acaaatgatccctgataagaaatgtaacgtgtgcttgaggtcttgagttacagataacttgca	1292
Db	1141	acaaatgatccctgataagaaatgtaacgtgtgcttgaggtcttgagttacagataacttgca	1200
OY	1293	agcgcataaaaaaatgtctcttcgcattccgcaattttccgaagaacagtgatattcca	1352
Db	1201	agcgcataaaaaaatgtctcttcgcattccgcaattttccgaagaacagtgatattcca	1260
OY	1353	gtgaagaatttgatgagatcatgagatgctgtgaggggtttccctgaagttgnaaaatgattg	1412
Db	1261	gtgaagaatttgatgagatcatgagatgctgtgaggggtttccctgaagttgnaaaatgattg	1320
OY	1413	gaaggaagaagtttgagaaggtgttttgcaagagcttgctgcgataagatgtcctagtcgaac	1472
Db	1321	gaaggaagaagtttgagaaggtgttttgcaagagcttgctgcgataagatgtcctagtcgaac	1380
OY	1473	aaggaagatctgagatgtaagaaacaaataatacatgtaagaagtttcatgagcttaataagac	1532
Db	1381	aaggaagatctgagatgtaagaaacaaataatacatgtaagaagtttcatgagcttaataagac	1440
OY	1533	ctgtgcgttgsagagagttccaagaaggagaaacattttatcatgaaagacatgtctctgac	1592
Db	1441	ctgtgcgttgsagagagttccaagaaggagaaacattttatcatgaaagacatgtctctgac	1500
OY	1593	gtatcatatccagaatgtttcatatctctgtatgtaaaatgagcccttaagaacgggtg	1652
Db	1501	gtatcatatccagaatgtttcatatctctgtatgtaaaatgagcccttaagaacgggtg	1560
OY	1653	actggtgataaataatattatgtccctatggtcttctaagaagctctcttcaaccctgta	1712
Db	1561	actggtgataaataatattatgtccctatggtcttctaagaagctctcttcaaccctgta	1620
OY	1713	aatgcatagttgagagatcatgacaaacaaactctttgaaacgaaccatctcgttttc	1772
Db	1621	aatgcatagttgagagatcatgacaaacaaactctttgaaacgaaccatctcgttttc	1680
OY	1773	tcttttcatcttgagccttataattatgtgtcccaaatcagaaggtgtgttcatltaaaata	1832
Db	1681	tcttttcatcttgagccttataattatgtgtcccaaatcagaaggtgtgttcatltaaaata	1740
OY	1833	ctcgaagatcttggaagcttgagacacacagacagatgtgtgttccctccgagagataactaagc	1892
Db	1741	ctcgaagatcttggaagcttgagacacacagacagatgtgtgttccctccgagagataactaagc	1800
OY	1893	ctcaatccgtgttgagttgacatcatatggtttccagcctatggaatttcogagatgccccaaga	1952
Db	1801	ctcaatccgtgttgagttgacatcatatggtttccagcctatggaatttcogagatgccccaaga	1860
OY	1953	atttgcaagtttatggaatctgcagacatctatgtttcaacacggtttcgatcagatatataa	2012
Db	1861	atttgcaagtttatggaatctgcagacatctatgtttcaacacggtttcgatcagatatataa	1920
OY	2013	attttctgaagaaatttgaggaacaaatgaagcaataaagcacttaaaactcccaagatt	2072
Db	1921	attttctgaagaaatttgaggaacaaatgaagcaataaagcacttaaaactcccaagatt	1980
OY	2073	tatttgcagagatgtcccaagtgagatctggttgcaaaaggaagacacttgatattttcaac	2132
Db	1981	tatttgcagagatgtcccaagtgagatctggttgcaaaaggaagacacttgatattttcaac	2040
OY	2133	tttcaaaactatttctactgtgctcccaagttgtgtgcaagaaagggttatatgvggagatt	2192
Db	2041	tttcaaaactatttctactgtgctcccaagttgtgtgcaagaaagggttatatgvggagatt	2100
OY	2193	cagaatgtccaanaaatlttagaaatcgatgtaaaataaggaatgacatgtaaaagtttccggac	2252
Db	2101	cagaatgtccaanaaatlttagaaatcgatgtaaaataaggaatgacatgtaaaagtttccggac	2160
OY	2253	tctgggcttcccaacaactctgtctatctgcagcaacttgaataatgagctctatatct	2312
Db	2161	tctgggcttcccaacaactctgtctatctgcagcaacttgaataatgagctctatatct	2220

QY	2313	gtcgattataagccttttgcagtgatcatcttaagttgcaaaagcgtttccagcaagctc	2372
Db	2221	gtgattataagccttttgcagtgatcatcttaagttgcaaaagcgtttccagcaagcgtc	2280
QY	2373	aagaagttaagtttgaaagaactatctaaagctgctgcaaaccttgagatcataagctgag	2432
Db	2281	aagaagtttgaagtgttgaaagaactatctaaagctgctgcaaaccttgagatcataagctgag	2340
QY	2433	ttgcctaaccttgaagtgctgtaagctgatagtaagtaagcgttgtgtgtgtaagaatgagcat	2492
Db	2341	ttgcctaaccttgaagtgctgtaagctgatagtaagtaagcgttgtgtgtgtaagaatgagcat	2400
QY	2493	ccaattgttatgtggatttaatcgattgaagcctttgtcctaataatataagttttctcaag	2552
Db	2401	ccaattgttatgtggatttaatcgattgaagcctttgtcctaataataatataagttttctcaag	2460
QY	2553	ttctctgaaagccacacaatgacacatttctctgtcctcttgagcgccatgattagaagttgc	2612
Db	2461	ttctctgaaagccacacaatgacacatttctctgtcctcttgagcgccatgattagaagttgc	2520
QY	2613	aaaaatttgaaagagatacccatgtagtttgagatalacacacatacagctgattgag	2672
Db	2521	aaaaatttgaaagagatacccatgtagtttgagatalacacacatacagctgattgag	2580
QY	2673	ttaagaagagtgctccctcccaaatcttgaggaaatctgctgcagaqaatttcgaagaagaacagaa	2732
Db	2581	ttaagaagagtgctccctcccaaatcttgaggaaatctgctgcagaqaatttcgaagaagaacagaa	2640
QY	2733	gacccctggaacaacaccctgtgattctgctatctcaatccatgaaagagagatgattct	2792
Db	2641	gacccctggaacaacaccctgtgattctgctatctcaatccatgaaagagagatgattct	2700
QY	2793	gattcagaagaacattag	2810
Db	2701	gattcagaagaacattag	2718
RESU.T. 6			
AA250262	ID	AA250262 standard; DNA; 2739 BP.	
XX	AC	AA250262;	
XX	DE	18-MAY-2000 (first entry)	
XX	XX	Coding region of potato Gpa2 resistance gene.	
XX	XX	Resistance gene; Gpa2; potato; phytopathogenic nematode; chromosome 12p	
KW	KW	marker; RPM4c; 111R; Potato Cyst Nematode; PCN; Globodera; nematolide;	
KW	KW	nematode resistance; detection; diagnosis; ds.	
OS	OS	Solanum tuberosum.	
XX	XX		
FH	FH	Key	Location/Qualifiers
FT	FT	CDS	1..2739
FT	FT		/*tag= a
FT	FT		/product= "Potato Gpa2 polypeptide"
FT	FT		/function= "Confers resistance to phytopathogenic
FT	FT		nematodes of the Globodera genus"
PN	PN	W0200006754-A2.	
XX	XX		
PD	PD	10-FEB-2000.	
XX	XX		
PE	PE	30-JUL-1999;	99WO-NL00491.
XX	XX		
PR	PR	31-JUL-1998;	98WO-NL00445.
XX	XX		
PA	PA	(CPRO-) CPRO-DLO CENT PLANTENVERDEELINGS REPROD.	
PA	PA	(UYWA-) LANDBOUWUNIVERSITEIT WAGENINGEN.	
XX	XX		
PI	PI	Van Der Vossen EAG, Van Der Voort JNAMR, Lankhorst RMK, Bakker J;	

PI Stiekema WJ;  
 XX WPI: 2000-18133/16.  
 DR P-PSDB; AAY44818.  
 XX  
 PT New isolated Gpa2 nematode resistance gene from potato, useful for  
 PT producing plants which are resistant to nematodes and polypeptides for  
 PT use in nematocidal compositions  
 XX  
 PS Claim 62; Fig 3a; 96pp; English.  
 XX  
 CC The present DNA sequence is the coding region of the potato resistance  
 CC gene Gpa2, that confers resistance to infection by phytopathogenic  
 CC nematode of the Globodera genus. It is mapped to short arm of chromosome  
 CC 12 (12P), between the markers IPM4c and 111R. This locus is associated  
 CC with resistance to Potato Cyst Nematodes (PCN) like G. pallida and  
 CC G. rostochiensis, that invade and damage the roots of Solanaceae. It has  
 CC nematocidal activity. A recombinant DNA sequence comprising the Gpa2  
 CC gene sequence can be transformed or transfected into plants, to provide  
 CC increased resistance to nematodes. The polypeptides can also be used in  
 CC nematocidal compositions and for detection and diagnosis of nematode  
 CC infections.  
 CC  
 XX  
 SQ Sequence 2739 BP; 814 A; 498 C; 600 G; 827 T; 0 other;

Query Match 8.8%; Score 272.8; DB 21; Length 2739;  
 Best Local Similarity 54.7%; Pred. No. 1.7e-61;  
 Matches 733; Conservative 0; Mismatches 567; Indels 45; Gaps 8;

QY 232 ttgtcagaacatttgagaaacaatgttttgggaaatgacggaatttgaagtagag 291  
 DB 113 tggagaacatcctgcaatataatgagcgatgaggggttaacaatcttggaagttagaa 172  
 QY 292 taagaagaattgcaagtgctgtcaatacacaaattcaactgagactaacaggaactgtca 351  
 DB 173 tcatagaggtgagcaatacaacagaagatagtggtgactcgaaatcaagaattgttttt 232  
 QY 352 tggagaagaataaagaacagaaagaagggcgctggaaggttcgtcaaaagcctgcgaac 411  
 DB 233 taagacaggaatgtggtgaaagaagcagggctatgtggtggaatttttgcgtctggagac 292  
 QY 412 aagtagagaagagacatgcatatcttgaaagagctgcgaagaagatccaagaataaagaa 471  
 DB 293 aagacactagaatgattgattccacgctgaaacagtgatgacacatcgacacagatga 352  
 QY 472 aacaagatcaagaagatcattgttcatatgatttcaagttcaacaagaattttga 531  
 DB 353 aagatctcaaaacccaactagctcactgtcagtttaacctgaac--atgattgtgagc 409  
 QY 532 aggttaagaacaatatgttgagctgagtgatgtaacaagaacagttgttaagaatctga 591  
 DB 410 agcccgagaatataatgtgttggccgtgaaatgaatttgaatgattcgtgatacaacttg 469  
 QY 592 ctagaagctactctggygaacccaagtcacccgaattgttcggaatggtggaagataagta 651  
 DB 470 ctagaagc---aggaagggaactagaaggtgtgtcacaatcgtagggagtgacatcgga 526  
 QY 652 aaaaacacctagcaaaaagagtttaacaatgataatcaattctatgacctgtttgatgttc 711  
 DB 527 aaaaacatttggctgcaaaaactctatagttactccttaattatgtctcgattatgatatc 586  
 QY 712 atgcttggttaccatatactcaacagcaacaagaagaattttgtcgtgaccttcgc 771  
 DB 587 gtgcaaaagcaactgttcaacaagaagatgtgtgagaagaatgtaactcctaagcctcttc 646  
 QY 772 attcacaatcaaatgagatgacaggggttaagatgattgtggaagcagagtagacagaa 831  
 DB 647 ctgtgacaagtgatgaacctgattatc-----agctagcggagcc 685  
 QY 832 tgttaacgaaaagttaagaagagaaggtactaatgttctgtgatatctgaggtt 891  
 DB 686 aactgcaaaagcatctgaaagcagagatactgtgtagtcatgtgacatcatgagacta 745

QY 892 gtgaagtgtgagatgagcgtagaacgattcttccaaactgaagaacaatgcagggaatcgaa 951  
 DB 746 cagaagcttgagatgatatataaactatgtttccca--gactgcgataatggaagcagaa 802  
 QY 952 tactgtgactaacccgtatagatgaagtagctgttatgctggtgtgtagaagaattttctt 1011  
 DB 803 tactctgactactcgcgaattgtggaatggtgcgaattatgactgacctgagctctctc 862  
 QY 1012 tggagatgacttcaatgataagaatgagatgttgagcttttcaaaagtgcagactttt 1071  
 DB 863 atcacatgacctcaatgataatttgcgaagaatgtgaaatttactacacaaaagatcttg 922  
 QY 1072 caagtgaag---cattacataatgagctgcgagactgtggaagaacatgcagatgaat 1128  
 DB 923 aaaaagaaggttctattctctctcgtgatttgaataattggaagaacaaattgtttaaat 982  
 QY 1129 gtcaaggttaccactaaactatgtcgtgtgtgcaggacctct--caacttaagaaga 1185  
 DB 983 gtgaggggttaacctagcaattacttgatgtgctgaccttctcccaaatcaglaaaa 1042  
 QY 1186 caatagaagattggaagaacttctgttaagaatgtcaagtcactgtctcaaatgtactctg 1245  
 DB 1043 catggaatgagtggaacaaatgctgcgagaatgtacgttcggtgtaagcagaatcttg 1102  
 QY 1246 atgaacgatgtcaacgtgtgtctggtgtgagttacatgacttgcgaagcgaatcctaaa 1305  
 DB 1103 aagcaaaatgcatgagaatgtgtgcttgaattacacactgtctctcccaaaac 1162  
 QY 1306 catgtctctgcaattcgaatttttccagaagacatgataatccagtgaagaatttga 1365  
 DB 1163 cgtgtttctgatttcaatttctgcagagatgaaacgagattatgttaataaacttg 1222  
 QY 1366 tgaatcatgagatgagctgaggggttccgca-----agttgaaatgatttgggaagag 1419  
 DB 1223 ttgagttatggccgtgagaggggtttttgaatgaagaagaggaagaagaagagag 1282  
 QY 1420 aggtttgaagaattgttgaagaagctgtgcagatagatgtcctgctgcagcaagagaa 1479  
 DB 1283 tggcagaacatgtataaagcaactgtgtagatagaagcttaattctatccacaatgtga 1342  
 QY 1480 gtcaagatgacaacaaaatagatcatgttaaggttcatgatcataatagacgtgtgcg 1539  
 DB 1343 gttttagtggggaaacacagag---atgtggaatgcagatgtgacccgtgaactctgt 1399  
 QY 1540 tgaagaagaatcagaagggaacattttta 1569  
 DB 1400 tgaagggaagctcgaaacatgaatttltga 1429

RESULT 7  
 AA250652  
 ID AA250652 standard; DNA; 2817 BP.  
 XX  
 AC AA250652;  
 XX  
 DT 23-MAY-2000 (first entry)  
 XX  
 DE Coding region of potato Gpa2 resistance gene.  
 KW Resistance; Gpa2; potato; phytopathogenic nematode; chromosome 12P;  
 KW marker; IPM4c; 111R; Potato Cyst Nematode; PCN; Globodera; nematocidal;  
 KW nematode resistance; detection; diagnosis; transgenic plant; ds.  
 XX  
 OS Solanum tuberosum.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..2817  
 FT /frag= a  
 FT /product= "Potato Gpa2 polypeptide"  
 FT /function= "Confers resistance to phytopathogenic  
 FT nematodes of the Globodera genus"



KM	nucleotide binding site; leucine rich repeat; pathogen resistance;
KM	plant; ss.
XX	
OS	Solanum tuberosum.
OS	Synthetic.
XX	
FH	
FH	key
FT	Location/Qualifiers
FT	37..2850
FT	/tag= a
FT	/product= "Modified resistance protein 25"

PN WO200129239-A2.  
 XX  
 PD 26-APR-2001.  
 XX  
 PF 12-OCT-2000; 2000WO-GB03930.  
 XX  
 PR 15-OCT-1999; 99GB-0024483.  
 XX  
 PA (PLAN-) PLANT BIOSCIENCE LTD.  
 XX  
 PI Bendahmane A, Baulcombe DC;  
 DR WPI; 2001-290924/30.  
 DR P-PSDB; AAU02143.  
 XX  
 PT Modifying activation characteristics of plant resistance proteins to  
 PT produce autoactivator polypeptide capable of activation in absence of  
 PT elicitor, by introducing modifications in amino acid sequence of  
 XX protein -  
 XX  
 XS Disclosure; Page 46-60; 77pp; English.

The sequence represents the coding sequence of Rx clone 25, a modified resistance activator. Rx encodes an NBS-LRR polypeptide having a nucleotide binding site (NBS), leucine rich repeat (LRR), and which mediates cellular response leading to pathogen resistance and/or cell death or dysfunction in response to an elicitor. The Rx was modified by introducing modification to the amino acid sequence to produce an autoactivator polypeptide, capable of activation in absence of an elicitor. Decoupling of resistance response from its natural elicitor is useful for developing novel pathogen resistant plants. The modified resistance proteins are useful for conferring resistance to non-natural agents or stimuli and also for investigating resistance response pathways and protein interactions e.g. with activators and repressors.

Sequence 3683 BP; 1149 A; 635 C; 782 G; 1117 T; 0 other;

SQ Sequence 3683 BP; 1149 A; 635 C; 782 G; 1117 T; 0 other;

	Query Match	8.8%;	Score 272.8;	DB 22;	Length 3683;	
	Best Local Similarity	54.7%;	Pred. No. 2e-01;			
	Matches 738;	Conservative 0;	Mismatches 567;	Indels 45;	Gaps 8.	
OY	232	tgttccaagaactcttgagaaaaacaatgltttttgggaaatgcacggatttgaagttaggy	291			
Db	149	tggsgaataccttcgaatatatayggcgatcatbgagggttaacaactcttggaagittgaa	208			
OY	292	taagagaagttgcacagtgctgtgaatacaaatccaactcgaactcgaactaacaggaattgac	351			
Db	209	tcgtaagyggtgcataccaccacagaagataagtttgtactcggaaaccaagaattgttttt	268			
OY	352	tgggagaaaataaagccagaaaaaaaagcgcgctgcgaagtttcgtlcaaagcctgcgaac	411			
Db	269	tagcacacgaatttggagagaaagacgacggcgctatgtggagaatttttcgctccggaac	328			
OY	412	aagtagcaggaatcgtgatcatatctcyaaaagatgcacaaagatcccaagataaagaa	471			
Db	329	aagcactcagaatlgcatgtatgccacgcggaacacgttgatgacacatcgcgcacgatga	388			
OY	472	aacaagratcaaggaatcatctgtgtcatgatttttcaagttcaacaacagataltttga	531			
	389	aaggtccnaaaccccaaaactgcgtcgcttgcagtttacctg--acatgctgttgagc	445			



```

RESULT 9
AAZ50264
ID AAZ50264 standard; DNA; 10329 BP.
XX
XX AAZ50264;
XX
XX 18-MAY-2000 (first entry)
XX
XX Genomic DNA of potato Gpa2 resistance gene.
DE
XX Resistance gene; Gpa2; potato; phytopathogenic nematode; chromosome 12p;
XX marker; IPM4c; 11LR; potato Cyst Nematode; PCN; Globodera; nematode;
XX nematode resistance; detection; diagnosis; transgenic plant; ds.
XX
XX Solanum tuberosum.
XX
XX Key Location/Qualifiers
XX misc_signal 1..4874
XX /tag= a
XX /note= "Gpa2 regulatory region"
XX CDS 4875..7850
XX /tag= b
XX /product= "Potato Gpa2 resistance protein"
XX /note= "This region is specifically claimed"
XX exon 4875..7850
XX /tag= c
XX /number= 1
XX /tag= d
XX intron 7586..7822
XX /tag= e
XX /number= 1
XX /note= "Located within the coding region of Gpa2 gene"
XX exon 7823..7850
XX /tag= e
XX /number= 2
XX /note= "Includes the stop codon, TGA"
XX intron 7942..8053
XX /tag= f
XX /number= 2
XX /note= "Located in the 3' UTR of Gpa2 gene"
XX
XX WO200006754-A2.
XX
XX 10-FEB-2000.
XX
XX 30-JUL-1999; 99WO-NL00491.
XX
XX 31-JUL-1998; 98WO-NL00445.
XX
XX (CPRO-) CPRO-DLO CENT PLANTENVERDEDELINGS REPROD.
XX (UYMA-) LANDBOUMUNIVERSITEIT WAGENINGEN.
XX
XX Van Der Vossen EMG, Van Der Voort UNAMR, Lankhorst RMK, Bakker J;
XX Stiekema WJ;
XX
XX WPI; 2000-183132/16.
XX P-PSDB; AAY44818.
XX
XX New isolated Gpa2 nematode resistance gene from potato, useful for
XX producing plants which are resistant to nematodes and polypeptides for
XX use in nematode compositions
XX
XX Claim 62; Fig 3c; 96pp; English.
XX
XX The present sequence is the genomic DNA of the potato resistance
XX gene Gpa2, inserted in the pBINRG2 plasmid. This plasmid is used to
XX transform host plant cells to produce transgenic plants. Gpa2 confers
XX resistance to infection by phytopathogenic nematode of the Globodera
XX genus. It is mapped to the short arm of chromosome 12 (12p) between the
XX markers IPM4c and 11LR. This locus is associated with resistance to
XX potato Cyst Nematodes (PCN) like G. pallida and G. rostochiensis, that
XX invade and damage the roots of Solanaceae. It has nematocidal activity.
XX A recombinant DNA sequence comprising the Gpa2 gene sequence can be
XX transformed or transfected into plants, to provide increased resistance

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CC to nematodes. The polypeptides can also be used in nematocidal
CC compositions and for detection and diagnosis of nematode infections.
XX
XX Sequence 10329 BP; 3150 A; 1542 C; 1924 G; 3713 T; 0 other;
SQ
Query Match 8.8%; Score 272.8; DB 21; Length 10329;
Best Local Similarity 54.7%; Pred. No. 3.1e-61;
Matches 738; Conservative 0; Mismatches 567; Indels 45; Gaps 8;
QY 232 ttgtcaagaactttgagaaacaatggttttggggaatgacgagatttgaagtgaag 291
DB 4987 ttggaagaatcttcaatataatggtcgtatcatgaggggttaacaatcttgaagttgaa 5046
QY 292 taagagaagtctgaagtgctgctgatacaacaattcaactgagactcaacggaactgtac 351
DB 5047 tcaatagaggtagcatatacacacagaagatgtgtgaactcggatacaagaatgttttt 5106
QY 352 tgggaagaataaagaagccagaaanaaagcgctcgaaggtttcgtcaaaagcctgcaac 411
DB 5107 tagcaggaattgtggggaagaagcaggtctatgtggggatttttctgcttctggaac 5166
QY 412 aagtagcagagagacatgcatcatctctggaagaagtcogacaagaatccagaataagaa 471
DB 5167 aagcactagaaatgcatgtatccacgctgaaacagtggaagcacaatcggacaagatga 5226
QY 472 aacaagatcaagaagaatcatgtttcatgatttttcaagttcaacaacaacgataattga 531
DB 5227 aagatctaaacaacacacacagctcactctgtcgtttactctgaac---atgattgtgagc 5283
QY 532 aggttaagaacaataltgttgcgcgtgatacaagaagaaacagttgttgaagaatctga 591
DB 5284 agcccggaatataatgttgcgcgtgaaatgaatttgatgcatgcatgcatgcatgcatg 5343
QY 592 ctagaagctactctcggggaacccaagtcacccgatttgcggatgagggagagatagta 651
DB 5344 ctagaag---aggaaggaactagaagtgcttccaacgtaggaagggagagacccgga 5400
QY 652 aaacaaccttagcaagaagtttaccatgatcatatcatcattccgcttctgattgttc 711
DB 5401 aaacaacttggctgcgaacaactctatagtgatcttaccatcatgctcgtattgtatcatc 5460
QY 712 atgcttgggtaccatattctcaacagcacaacaanaagaaatttgcgtgctcttcgc 771
DB 5461 gtgcgaagaagcaactgttccaagaagatgtgtgaaatgtaacccctagcctctctt 5520
QY 772 attccacaatcaaatgtagacaggggttaagatgtattgttgagaagcagagctcagaa 831
DB 5521 ctttgacaagtgatgaaacctgattatc-----agctagcggagcc 5559
QY 832 tgttacagaagaagtttaagaagaagaggtacttaattgtcttgatgatactcgaagt 891
DB 5560 aactgcgaagaagcatctgaagaagcagagatacttggtagcatattgatatgatactgata 5619
QY 892 gtgaagtgtggatgagcgtgagacgaltgttccaactgagaagaatcaggaagtcgaa 951
DB 5620 cagaagcttggatgataataaactatgttccca---gactcgtataatgagaagcagaa 5676
QY 952 tactgtgactaccgcgaatgagatgagtagctgttatgtctgtgtgagaagaattttct 1011
DB 5677 tactccctgactaccgcgaatgagatgagtagctgttatgtctgtgtgagaagaattttct 5736
QY 1012 tgcgtagtcatatgataagatgagatgaggttggagttctttcaaaagtgcagcatltt 1071
DB 5737 atcacatgagcgcctcatgatttgaacgaagaagtttgaaatttactacaacaaagaatcttc 5796
QY 1072 caagtgaag---catccatagatgagtcgagacgttggaaagcaaatcgcagatgaat 1128
DB 5797 aaaaagaaggttctatctccctgaatttgaataatttggaaacaacaatgacttaaat 5856
QY 1129 gtcaacggttaccactactactgttctgtgttgcagggcttc---caatctaaagaa 1185
DB 5857 gtggaaggttaccctctagcaattacttgcgtgacttctcctcaaatcagcaaaa 5916

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[illegible][illegible]

Recombinant *Gpa2* polynucleotide from potato, *Solanum tuberosum*, useful to confer resistance to phytopathic nematodes of the genus *Globodera* in transgenic plants, e.g. resistance to potato cyst nematodes in potatoes

Claim 21; Fig 3c; 96pp; English.

The present sequence is the genomic DNA encoding potato *Gpa2* resistance protein. It is inserted in the pKIN62 plasmid which is used to transform host plant cells to produce transgenic plants. *Gpa2* confers resistance to infection by phytopathogenic nematode of the *Globodera* genus. It is mapped to short arm of chromosome 12 (12p), between the markers IPM4 and 11R. This locus is associated with resistance to potato Cyst Nematodes (PCN) like *G. pallida* and *G. rostochiensis*, that invade and damage the roots of Solanaceae. It has nematocidal activity. Recombinant DNA sequence comprising the *Gpa2* gene can be used to produce transgenic plants with increased resistance to nematodes. The polypeptides can also be used in nucleic acid compositions and for detection and diagnosis of nematode infections.

Sequence 10329 BP; 3150 A; 1542 C; 1924 G; 3713 T; 0 other;

Query Match	8.8%;	Score 272.8;	DB 21;	Length 10329;
Best Local Similarity	54.7%;	Pred. No. 3.1e-61;		
Matches 738; Conservative	0;	Mismatches 567;	Indels 45;	Gaps 8;

QY	232	ttgtcaagaactttgagaaaaacatgttttttggggaatgcggaatttgaagtagagg	291
Db	4987	tggagaaatcctgtcaataataatggtggtatcaggtatgagggttaacaacattggaaattgtaa	50486
QY	292	taaggaagtgtgcaagtgtgtgtgtgaatacaacaattcaactgagactaacaggaactgtac	351
Db	5047	tcatgaggtgtgcatacacacagaaagatltgttctgactcggaaatcaagaattttttt	51068
QY	352	tgggagaataataaagccgagaaaaaagagcggtcgaagtttgcgaagctgcac	411
Db	5107	tagcacggaatgtgtggaaaaaagacgaggtctatgtgggggttttttctgccttggaac	51668
QY	412	aagtagcagagagacatgcatcatctctggaagagtcgacaaagatcacagaataaagaa	471
Db	5167	aagcctcgaatgatgtattgtattccacgctggaacagtggatgtgcaacatcgcgaacatga	52268
QY	472	aacaagttcaagaagatcatctgtttcatatttccaagttcaacaacagcatatttga	531
Db	5221	aagatctaaacccaacaactcagctcgaactgttcaagtttaacctgaac---atgattgttgcg	52868
QY	532	aggttaagaacaataatgttggacgtgatatcaagaagaacagttgtttaagaagatctga	591
Db	5284	agcccgagaataataatgttgcgttgaataatgaatttgatgtagatgcgtgcgaatcattg	53438
QY	592	ctagaagctactcttgcggaacccaagttccaccgatttgcgagtagagagcatagta	651
Db	5344	ctaaagg---aggaagggaactagaagtgttcccatcgttagggataggagacacggga	54008
QY	652	aaacaaccttgcagaagaagatttacaatgaatgaatcaatctctatgcgttttagtgc	711
Db	5401	aaacaacttctgtgcaaaacatcctatgtatcttcaatttgaattgtctcgaattgttattc	54608

```

QY 712 atgctgggctaccatctcaacgacacaaagaaatttgcctggcctctgc 771
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 5461 gtgcacaaagcaactggttcacagagatgtgttgagaaatgactccctgagcctctt 5520
QY 772 attcccaatcaaatggtgacaggggttaagatgtgttgagaaagcagctgcagaa 831
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 5521 ctltgacaagtgtgacccgattatc-----agctagcggagc 5559
QY 832 tgttaagaaaatttaagaaagaggttaattctgttctgtgatactctgaggt 891
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 5560 aactgcacaaagcactgcgaagagagatactctgttactatgtatgacatagacta 5619
QY 892 gtgaagtgtgagatgagcgtgagacgactgtcccaactgaagacaatgcaggaatgcga 951
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 5620 cagaactgtgagatgataaactatgttccca---gactgcgataatgagagacga 5676
QY 952 tactgttgcactccgtaagtgtgagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1011
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 5677 tactcctgactcctcggaatgtggaagtgtgtaatactgactgactgactgactgactc 5736
QY 1012 tgcgagatgactgactgactgactgactgactgactgactgactgactgactgactgact 1071
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 5737 atcaactgagcctcactgactgactgactgactgactgactgactgactgactgactgact 5796
QY 1072 caagtgaag---cattacatatgagttcgagactgtgtggaagacaatgcagatgaa 1128
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 5797 aaaaagaaggttcttacttctcctgaatttgaaataatgtggaacaaattgcatlaaa 5856
QY 1129 gtaacgggttaccactaactatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1185
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 5857 gtggaaggttaccactaactaacttactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5916
QY 1186 caataagaatttgaaactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1245
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 5917 catgtgagatgagtgcaaaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5976
QY 1246 atgaacgagtgtcagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1305
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 5977 aagcaaaatgcatgagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6036
QY 1306 catgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1365
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 6037 cgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6096
QY 1366 tgaagatcagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1419
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 6097 ttgagatcagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6156
QY 1420 aggttgagaaagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1479
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 6157 tggcagaacacatgtataacgactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6216
QY 1480 gtgcagatgagacaaatagatcatgtaagtgttcagatcatatataatgacgtgtgcg 1539
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 6217 gttttgagtgaggaacacagag---atgtggaatcagatgagtgacccgtgaactctgt 6273
QY 1540 tgaagagaagtgtcaagggagacaatttcta 1569
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 6274 tgaaggaagctgcgaacatgaatttgcga 6303

```

## RESULT 11

AA237153  
ID AA237153 standard; DNA; 5820 BP.

AC AA237153;

DT 01-FEB-2000 (first entry)

DE DNA sequence of BAC77 including the potato Rx gene.

KM Potato; Rx gene; resistance gene; potato virus X; PVX; transgenic plant;  
broad spectrum extreme resistance; Narcissus mosaic virus; NMV; NVX; VMV;

```

KM Nandina virus X; Viola mosaic virus; Cymbidium mosaic virus; CYMV; PopMV;
KW Poplar mosaic virus; White clover mosaic virus; WCLMV; activate; ss.
OS Solanum tuberosum.
FH Key Location/Qualifiers
FT CDS 2248..5407
    /tag= a
    /product= Rx
    /note= "Resistance gene product"
FT exon 2249..4944
    /*tag= b
    /number= 1
FT intron 4945..5178
    /*tag= c
    /number= 1
FT exon 5179..5289
    /*tag= d
    /number= 2
FT intron 5290..5400
    /*tag= e
    /number= 2
FT exon 5401..5407
    /*tag= f
    /number= 3
PN MO954490-A2.
XX 28-OCT-1999.
PD 16-APR-1999; 99MO-GB01182.
XX 16-APR-1998; 98GB-0008083.
PR (PLAN-) PLANT BIOSCIENCE LTD.
XX Bendahmane A, Baulcombe DC, Kanyuka KV;
XX WPI: 1999-634006/54.
DR P-PSDB; AA52152.
XX New isolated plant virus resistance gene, used to produce transgenic
PT plants with resistance to virus infection.
XX Claim 4; Page 83-87; 124pp; English.
XX This is the DNA sequence of BAC77 which includes the potato Rx gene
CC between nucleotide residues 2248-5407. The Rx gene is a resistance gene
CC which confers extreme resistance against potato virus X (PVX). Sequence
CC AA237154 is the Rx coding sequence free from introns. The Rx gene can be
CC used to create a recombinant vector which encodes the Rx resistance
CC polypeptide AA52152, this vector can be used to transform plant cells
CC to produce a transgenic plant with resistance to PVX. The Rx gene can be
CC used to engineer resistance traits, preferably broad spectrum extreme
CC resistance, into plants. The Rx gene can also be activated by non-PVX
CC viruses, e.g. Narcissus mosaic virus (NMV), Nandina virus X (NVX), Viola
CC mosaic virus (VMV), Cymbidium mosaic virus (CYMV), Poplar mosaic virus
CC (PopMV) and White clover mosaic virus (WCLMV). Rx can be used to offer
CC specific protection against this group. The Rx gene sequence can be used
CC to create antibodies specific for Rx. The antibodies can be used to
CC down-regulate Rx activity and also for the detection, identification or
CC isolation of Rx or homologues.
XX Sequence 5820 BP; 1776 A; 996 C; 1111 G; 1937 T; 0 other;

```

Query Match 8.8%; Score 271.8; DB 20; Length 5820;

Best Local Similarity 48.9%; Pred. No. 4.5e-61;

Matches 1298; Conservative 0; Mismatches 1252; Indels 105; Gaps 17;

QY 232 ttgtcagaacttggaaacaaatgttttggggaatgcgagtttgaagtagag 291  
DB 2361 tggagaatcctgcgaataatgagcgatcagtaggggttaacaactcttgaa 2420

QY 292 taagaagaattgcgaatgctgtctataacacaaattcaactctgaactcaaggaactgtac 351  
DB 2421 tctgataaggtatgcatacaacagaagatatgttgactcggaaactgaagaatttttt 2480  
QY 352 tggagaagaataaagaagccagaagaaagcgctgcgaagtttcgtcaaaagcctgcac 411  
DB 2481 tagcaacgaatttggaggaagaagcagggtatgtgaggaaatttttctgccttgagac 2540  
QY 412 aagtaagcaggagacatgtatcatatctgaaagagtcgcaaaagatccaaagaaagaa 471  
DB 2541 aagcaactagaatgatttgattccacgctgaaacagtgatgcaacatcggacagcatga 2600  
QY 472 aacagaatcatcaagaagaatcatgttctatgtattttcaagttcaacaagaatatttga 531  
DB 2601 aagatctcaaaaacccaactcagctcgtctgtcgaatttaccctg---aaatattgttgagc 2657  
QY 532 aggttaagaacacatattgttgacgtgatagtcaagaagaacagttgttagaagatcga 591  
DB 2658 agcccggaataataatattgttgccgtgaaatgaaatttgaaatgatactgatacactgt 2717  
QY 592 ctagaagctactctggyggaaccacaagtcacccgattgtcggatggyggaagataagta 651  
DB 2718 ctagaag---aggaagggaaactagaagttgtctcaatcgtagaggatggygacatcgga 2774  
QY 652 aaaaacactagcaaaagaagtttacaatgataatcaattctatgcttctgattgttc 711  
DB 2775 aaaaacactgtgctacaaaactctatagttacgttgatctgtcattgtctgattgatactc 2834  
QY 712 atgctgtggtctacacatctcacaagcacaacaaaagaatattgttggtggtccttcgc 771  
DB 2835 gtgcaaaaagcaactgtttcacaagaagatattgtgagaagaatgtaactcctaagccttctt 2894  
QY 772 attccacaatcaaaatggaatgacaggtttaagatgattgttgaagcagagctagcagca 831  
DB 2895 ctttgacaagtgtacgaactgtat-----galtcagctagcagcacc 2933  
QY 832 tgttaacgaagaagtttaagaagaaggttacttaattgtcttgatgatatctcgagtt 891  
DB 2934 gactgcacaaaacatctgaaagcgagagatattgttgatcgtatgactacataagacta 2993  
QY 892 gtgaggtgtgagatgagcggtgagacatgcttccaaactgaaacatgcaagggatcgaa 951  
DB 2994 cagaagcttggagatagataataaactatgttccca---gactgttataatggaagcagaa 3050  
QY 952 tactgttgaactacccgtaatgataagtagctgttlatatgctgtgagagaatttttct 1011  
DB 3051 tactcctgaactacccgtaatgataagtagctgtgataatgactagttcagtaagcctcctc 3110  
QY 1012 tgcgagatgagcttatgtatcaagaatgagattgagttctttcaaaagtcaacattt 1071  
DB 3111 altcaatgtgcctcatgaattttgacgaagaattggaatttactacacaaaagaattcttg 3170  
QY 1072 caagtgaag---cattaccatagattcgagactgtttggaagaacaaatcgacatgat 1128  
DB 3171 aaaaagaaggttcttatcttctcctgaatttgaataatattggaaacaaattgcattaaat 3230  
QY 1129 gtcaaggtttacacactactatgtcgtgtgtgcaagggctct---caactctaaaagaa 1185  
DB 3231 gtggaagattaccctcctgaactactgtgattgtcgtgactctctccaaaatgtgtcaaa 3290  
QY 1186 caataagaagattggaanaactgttctaaagatgtcaagatcatctgtcaaaatgatactcg 1245  
DB 3291 gattagaattgagcaagaatgtgggaaatgtlaaagttcgtgtcgttgacagacatctgt 3350  
QY 1246 atgaacagatgtcacgtgtgtgtgtgagattagacatcactttgacaagcatcctaaaaa 1305  
DB 3351 aagcaacatgataagagtggt 3410  
QY 1306 catgtctctgcatctcgaaattttccagaagaacagtgatatactcagtgagaatttga 1365  
DB 3411 cgtgtttctgtatttttgcaattttcacaagagatgaaacagatttctgtaattgaaactgt 3470

QY 1366 tgagatcatgtatgctgtaggggtttccgta-----agttgaaatgatttggaaagag 1419  
DB 3471 ttgagttatgctgttagaaggtatttttgaattgaagaagagggaaagcaatagaagag 3530  
QY 1420 aggttgaagaattgttttcaagaagctctgcgataagatgtctcctcgtcgaagaagaa 1479  
DB 3531 tgcgaacacatgataaagcaacttataagataagagctttaaatttccatccacaatttta 3590  
QY 1480 gtcaagatggaacaaaatattgatactgtaaggttcaatgatacttaataatgacgtgtcg 1539  
DB 3591 gtttctggtggaacaaatagaag---ttgtggaatgcattgtgtgacccgtgaaactgtt 3647  
QY 1540 tgaagaagaattcgaaggaagacaatttta---tcaigaagacattgttcttgacgat 1596  
DB 3648 tgaagggaagctcgaacaaatgaaatttttgaattgttataaggaagaagattgatacaat 3707  
QY 1597 catatccagaattgttcatatctctgtatgataaataatgcaagcctttaaagcgtgagct 1656  
DB 3708 catgtgcacaatccatgacagcttccctttaaagatgcgaagatcggatcgaatcacaag 3767  
QY 1657 gtatgaaatataatattgtccctatgcttataaggtctctctta-----1704  
DB 3768 tgaagaattgtgtgtgtgtgtgaacagtgaggtcattcttatactatgtgtggtgat 3827  
QY 1705 -----ccctgttaaatcgttcaagttgagaggtcgaacacaaca--alttttga 1752  
DB 3828 tgaatgcgtacacactgtgaatgttcttcaagctagaagaatgataatcttgatttga 3887  
QY 1753 aagcaacacattctgttctcttcttcaactgtgaaccttataatatttctcaaatcag 1812  
DB 3888 atacatgccaatttttccagtgagatcatttcttcaattcatttgatgatactactt 3947  
QY 1813 aggtgttcaattcaaatctactcaagctctgtgagctaga-----cacgaacga 1863  
DB 3948 tgcgttttaactcctgtcttaacagcagatcaagagctcgaagaagcgttccctcatcaa 4007  
QY 1864 ttgattgttccctcctcagagataactcaagcctcaatcgtgtt-----agttacc 1911  
DB 4008 taatagacatccctcctacgatalataacagctatgtctatctgtaaaactttaaactaac 4067  
QY 1912 tatcatgttaagctatggaatttcgatagttaccctcgaagatttgcaggttatgaaatc 1971  
DB 4068 ttccatttccagttatatactcttcatataataacatcggaattttgacgagccacat 4127  
QY 1972 tgcagaacatcaattgttcaacgggttgcatacagataataaattttgtctgagaattt 2031  
DB 4128 tgagagacgtgtgtatgagctggaattactgtgcggaatgacatgagcctcagaagaacag 4187  
QY 2032 gggaactaatgcaatt---aaggcacttaaacgtcccaagatttattttgccaagttgc 2088  
DB 4188 tggtttgaanaaatttgcgaatgctccaatcaattgaacccctcgttatgttacaaggtctc 4247  
QY 2089 caagtgtatcgtttgacaagaagcacttgaatttttcaaaacta--caaactttct 2147  
DB 4248 tttttagactatttcccaatttaagaaggttgcgaagtttttggcgtcccaagaagcttcc 4307  
QY 2148 tactgttccaggtgtgtgcagaaggttlatatggttggtatcagaatgtcaaaaaa 2207  
DB 4308 gcaatagcgaagcctgtatgatatttgcacttatactacgtgcgaagaatgtacatttc 4367  
QY 2208 ttagaacatgtaagaataaagaatgatacatabaaagtttgcgactcgtggttcccaac 2267  
DB 4368 gttatataatcacaatagctgtgttcttcaaaaacacgtgcaacttcaagtttatacgc 4427  
QY 2268 aatctgtcctatctgcagcaacttgaanaatgtgaatgtatatactgtt-----gattata 2322  
DB 4428 aagatccctctgagtttcaagcgaagaatattgtcacaagaagattgatttgcggggaactg 4487  
QY 2323 gactttgacagtgatacttcaagtcaaaagcttccagcaagcgtcgaagaattga 2382  
DB 4488 caactccaacttactccttactcctccgagtgcttttccacaacaaacttaagaatttga 4547  
QY 2383 agtc---ggaaagaactatcatcgaactgtgtcatalacttggacatcatcagctagtgctcta 2439

Db 4548 ctttggggagagattctctgtgctgaggaagatttgacattgtgttaattaccaca 4607  
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 Db 4608 aactcagagctctatactatactatcagatgacgtcttcaaggaagtggaagtgtg 4667  
 QY 2500 ttatggatttaattcagattgaagctttgtcatttaataatagtttttccaagttcga 2559  
 Db 4668 aggaagaggttccctcagctgaagttctgttcttcgagatgattatacattcagatcga 4727  
 QY 2560 aagcccaaatgacaatttccctcgtctgtgagcgccctcagatgattgaagtgcacaatt 2619  
 Db 4728 gagctagtagtgcattccttcgtacgttgcagagagttatctttagagatttcgcgttaatt 4787  
 QY 2620 tgaagaagatataccattgattgttcagatatacacacactacagctgattgtaagag 2679  
 Db 4788 tggattcaatccctcagctgaattttgcagatataccacactagctcttattgatatagatt 4847  
 QY 2680 agtgcctcccaacttgagggaattctgctgcagcaatctagaagaacagagacctcg 2739  
 Db 4848 actgtcaacaatctgtgtggaattccgcaagcaaatctcaacagacattcaagacaact 4907  
 QY 2740 gaaacaacctgtgagtgctgtatctcaatccattgaagagagtgattctgattcag 2799  
 Db 4908 atggaagctctacgaggtccacactcgtcattcttgaagacattcttccctgtctt 4967  
 QY 2800 aagaacattaggaat 2814  
 Db 4968 tacacaataatata 4982  
 RESULT 12  
 AAZ37154  
 ID AAZ37154 standard; cDNA; 3066 BP.  
 AC AAZ37154;  
 DT 01-FEB-2000 (first entry)  
 DE Partial nucleotide sequence of Rx gene cDNA.  
 XX  
 KW Potato; Rx gene; resistance gene; potato virus X; PVX; transgenic plant;  
 KW broad spectrum extreme resistance; Narcissus mosaic virus; NMV; NVX; VMV;  
 KW Nandina virus X; Viola mosaic virus; Cymbidium mosaic virus; CYMV; PopMV;  
 KW Poplar mosaic virus; White clover mosaic virus; WCIMV; activate; ss.  
 XX  
 OS Solanum tuberosum.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..2864  
 FT /tag= a  
 FT /Product= Rx  
 FT /note= "Resistance gene product"  
 XX  
 PN WO954490-A2.  
 XX  
 PD 28-OCT-1999.  
 XX  
 PF 16-APR-1999; 99WO-GB01182.  
 XX  
 PR 16-APR-1998; 98GB-0008083.  
 XX  
 PA (PLAN-) PLANT BIOSCIENCE LTD.  
 XX  
 PI Bendahmane A, Baulcombe DC, Kanyuka KV,  
 DR WPI, 1999-634006/54.  
 DR P-PSDB; AAY52152.  
 XX  
 PT New isolated plant virus resistance gene, used to produce transgenic  
 PT plants with resistance to virus infection -  
 XX

PS Claim 4; Page 87-90; 124pp; English.  
 XX  
 CC This is the DNA sequence of the potato Rx gene. The Rx gene is a  
 CC resistance gene which confers extreme resistance against potato virus X  
 CC (PVX). Sequence AAZ37153 is the Rx gene including introns. The Rx gene  
 CC can be used to create a recombinant vector which encodes the Rx  
 CC resistance polypeptide AAY52152, this vector can be used to transform  
 CC plant cells to produce a transgenic plant with resistance to PVX. The Rx  
 CC gene can be used to engineer resistance traits, preferably broad spectrum  
 CC extreme resistance, into plants. The Rx gene can also be activated by  
 CC non-PVX viruses, e.g. Narcissus mosaic virus (NMV), Nandina virus X  
 CC (NVX), Viola mosaic virus (VMV), Cymbidium mosaic virus (CYMV), Poplar  
 CC mosaic virus (PopMV) and White clover mosaic virus (WCIMV). Rx can be  
 CC used to offer specific protection against this group. The Rx gene  
 CC sequence can be used to create antibodies specific for Rx. The antibodies  
 CC can be used to down-regulate Rx activity and also for the detection,  
 CC identification or isolation of Rx or homologues.  
 CC  
 SQ Sequence 3066 BP; 913 A; 533 C; 675 G; 945 T; 0 other;

Query Match 8.7%; Score 269.6; DB 20; Length 3066;  
 Best Local Similarity 54.5%; Pred. NO. 1.3e-60;  
 Matches 736; Conservative 0; Mismatches 569; Indels 45; Gaps 8;

QY 232 ttgtcaagaacttgagaaacaattttttgggaatgacgagatttgaagtagag 291  
 Db 163 tggagaaatcctgtcaatatatggtggtatcgtggtggttaacattcttgaggtgaa 222  
 QY 292 taaggaagttgcaagtgtgtgtatatacacaattcaactgagactacaggaactgtac 351  
 Db 223 tcttagaagtagcatacacacaagaatagtgtgactcggaatcagaagaattgtttt 282  
 QY 352 tggagaaataataaagccagaaagagcgctgcaaggttttcgccaagcctgcaac 411  
 Db 283 tagcagaatttggaggaagaagacggtctatgtgtgagatttttgcgtcctggaac 342  
 QY 412 aagtagcagagagatgcatatcttggaagaagtcgacaagaatccaagataaagaa 471  
 Db 343 aagcactagatgattgtatccacgtgaacagtgatgagcaacatcgacagcagcga 402  
 QY 472 aacaagtatcaaaagatcatgtgttcatgtatttttcaagtcaacaagaatatttga 531  
 Db 403 aagatcttaaacccacaactagctgcgttgcagtttaacccg---aacatgagtgtgagc 459  
 QY 532 aggttaagaacaatatgtgtgagctgagatgatacaagaaacagttgttagaagatcga 591  
 Db 460 agcccgagaatatatgtgtgtggtccgtgaagaatttgatgattgctgtgataacttg 519  
 QY 592 ctagaagctactctggtggaacccaagtcatcccgattgtcggagtgagggacatagta 651  
 Db 520 ctagaag---aggaagggaaactagaagttgtctcaactcgttaggtatggagacatcgga 576  
 QY 652 aaacaaccttagcaaaagaaagtttacaatgtagtaataattctatgscgtttgattgt 711  
 Db 577 aaacaacttggctacaacaactcatatgtgtgtccgtgtcatattgtccgatttgatattc 636  
 QY 712 atgcttggtctacatatctcaacagcacaacaagaagaatttgcctggtcccttcgc 771  
 Db 637 gtgcaaaagcaactgtttcacaagaagatattgtgtgagaatgtactccttagcctcttc 696  
 QY 772 attcacaatacaaaatgtagacaggggttaagatgattgttgaagcagagactcgagaca 831  
 Db 697 cttagacagtgatgaactgtat-----gatacagctagcggacc 735  
 QY 832 tgttaacgaaagtttaagagaaaggttacttaattgtcttgatgatatctgaagtt 891  
 Db 736 gactgcaaaagcacttgaaagcaggaagtaactgtgttagtcatatgtagacatattgacta 795  
 QY 892 gtgaagtgagatgagcgttgagacgagcttcccaactgagaacaatgacagaggtgcga 951  
 Db 796 cagaagcttgtagatataaaactatgtttccagagctgtataat---ggaagcagaa 892

QY 952 tactgttactaacocgtaagatgaatgaatgttactgtgtgtgtagaagattttctt 1011  
 DB 853 tactcctgactactcgtgaagatgtgaagctgtaactgtactgtacgaagcctctc 912  
 QY 1012 tgcgagatgactatgatacaagatgagatgttgaagcttcttcaaaagtgcagattt 1071  
 DB 913 atcaatagcgcctcattgaatttgcagaaagtgttgaatttactacacaaaaagcttctg 972  
 QY 1072 caagtgaag--cattacatagatgtcgagactgttgaagaacaaatgcagatgaat 1128  
 DB 973 aaaaagaagttcttactatccctgaatttgaataatttgaacaaatgtcattaat 1032  
 QY 1129 gtcaagggttaacactactactgtgtgtgtgtgagggcttct--aaatctcaaaagga 1185  
 DB 1033 gtgagagattacactctgaactactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1092  
 QY 1186 caataagaagattggaacactgttgcataaagatgtcaagtcattctcacaatgatctgt 1245  
 DB 1093 gattagatgagtggaagaaatgtggaagaaatgtgaagtcgtgtgtgtgtgtgtgtgtgt 1152  
 QY 1246 atgaagatgttcaagtggt 1305  
 DB 1153 aagcacaatgcatgagatgt 1212  
 QY 1306 catgtctctgcattctgcgaatttccagaagaagcagtgatctcagtgagaagatttga 1365  
 DB 1213 cgtgttctcgtatcttgcgaatttccagaagaagcagtgatctcagtgagaagatttga 1272  
 QY 1366 tgaagatcatgagatgt 1419  
 DB 1273 ttgagatgtgagcgt 1332  
 QY 1420 aggttgaagatgt 1479  
 DB 1333 tggcaacaacatgataacttaagataagatgaagcttaatttcaatccacaatttga 1392  
 QY 1480 gtgcagatgtggaacaaatgaatgatactgtgaagtcgtgtgtgtgtgtgtgtgtgtgt 1539  
 DB 1393 gtttctgtggaacaaatgaag--ttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1449  
 QY 1540 tgaagagaatgtcaaaagggagacaatttga 1569  
 DB 1450 tgaagagaatgtcaaaagggagacaatttga 1479

RESULT 13  
 AAS03715  
 ID AAS03715 standard; cDNA; 3014 BP.  
 XX  
 AC AAS03715;  
 XX  
 DT 29-AUG-2001 (first entry)  
 XX  
 DE DNA encoding Rx 72, a modified resistance protein.  
 XX  
 KW Rx: modified resistance; NBS; LRR; cell death; autoactivator;  
 KW nucleotide binding site; leucine rich repeat; pathogen resistance;  
 KW plant; ss.  
 XX  
 OS Solanum tuberosum.  
 OS Synthetic.  
 XX  
 FT Key Location/Qualifiers  
 FT CDS 42..2855  
 FT /\*tag= a  
 FT /product= "Modified resistance protein 72"  
 PN WO200129239-A2.  
 XX  
 XX 26-APR-2001.  
 PD  
 PF 12-OCY-2000; 2000MO-GB03930.  
 XX

PR 15-OCY-1999; 99GB-0024483.  
 XX  
 XX (PLAN-) PLANT BIOSCIENCE LTD.  
 PA  
 PI Bendahmane A, Baulcombe DC;  
 XX  
 XX WPI: 2001-290924/30.  
 DR P-PSDB; AAU02145.  
 XX  
 XX Modifying activation characteristics of plant resistance proteins to  
 PT produce autoactivator polypeptide capable of activation in absence of  
 PT elicitor, by introducing modifications in amino acid sequence of  
 PT protein -  
 XX  
 PS Disclosure; Page 46-57; 77pp; English.  
 XX  
 XX The sequence represents the coding sequence of Rx clone 72, a modified  
 CC resistance autoactivator. Rx encodes an NBS-LRR polypeptide having a  
 CC nucleotide binding site (NBS), leucine rich repeat (LRR), and which  
 CC mediates cellular response leading to pathogen resistance and/or cell  
 CC death or dysfunction in response to an elicitor. The Rx was modified by  
 CC introducing modification to the amino acid sequence to produce an  
 CC autoactivator polypeptide, capable of activation in absence of an  
 CC elicitor. Decoupling of resistance response from its natural elicitor is  
 CC useful for developing novel pathogen resistant plants. The modified  
 CC resistance proteins are useful for conferring resistance to non-natural  
 CC agents or stimuli and also for investigating resistance response pathways  
 CC and protein interactions e.g. with activators and repressors.  
 XX  
 SQ Sequence 3014 BP; 891 A; 555 C; 674 G; 894 T; 0 other;

Query Match 8.6%; Score 268; DB 22; Length 3014;  
 Best Local Similarity 54.4%; Pred. No. 3,4e-60;  
 Matches 735; Conservative 0; Mismatches 570; Indels 45; Gaps 8;

QY 232 ttgtcagaacttgcagaaacaaatgttggggaatgacgatttgaagtagagg 291  
 DB 154 tggagaatctctgcaatataatgtggtgcatgaggggttaacaatcttggaagtgtgaa 213  
 QY 292 taagaagaatgtcgaagt 351  
 DB 214 tctgtagagtgatgatacacaagaagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 273  
 QY 352 tggagaagaataaagccagaagaaagagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 411  
 DB 274 tagcacagaattgtgaggaagaagcaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 333  
 QY 412 aagtagcagagatgatactgtgaagaagtcgacaaagatcccaagataaagaa 471  
 DB 334 aagcactagaatgtcatgtatccacgtgaacagtgatgtgcaacatcgacagatgaa 393  
 QY 472 aacaagatcaaaagaaatcattgt 531  
 DB 394 aagatctaaacccaacaaactagctgt 450  
 QY 532 aggttaagaacaaatgt 591  
 DB 451 agcccgagaatataatgt 510  
 QY 592 ctagaagctactctgtggaacccaagatcccgatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 651  
 DB 511 ctagaag--aggaagggaaactagaagtgctcactatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 567  
 QY 652 aaacaacctagaagaagaagttcaaatgataatcattatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 711  
 DB 568 aaacaacttgcatacaaaactctatagtagtccgt 627  
 QY 712 atgctgt 771  
 DB 628 gtgcagaagaacgt 687  
 QY 772 attccacaatcaaatgataagtagaggttgaagatgt 831

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Db      688      cttgcaagatgtagaccgat-----gattcagctagcgacc 726
QY      832      ttttaacaaagaatttaagaagaaggaactaattgtcttgatgatctgagtt 881
Db      727      gactgcaaaagacatccggaagcagagatacttgtagcatgtgatgatgacta 786
QY      892      gtgaagtgtggaatgagcgtgagacgagtgcttccaactgaaacatgacggagtcgaa 951
Db      787      cagaagcttgagatgataaaactatgttcccgacgctataat---ggaagcagaa 843
QY      952      tactgttgacacccgataatgataatgagctgttactgtgtgtagagaattttctt 1011
Db      844      tactctgactactcgaatgtggaagtgtcgaatattcgaatgtaagcagccctc 903
QY      1012      tgcgagtgagcttcagatgagatgagattgagctcttcacaaagtcagcagcttt 1071
Db      904      atcactcgcgcctcagatatttgacgaaagttggaattactacacaaagaattcttg 963
QY      1072      caagtgaag---cattacataatgagtcgagactgttgaaagcaaatcgacagatgat 1128
Db      964      aaaaagaagatcttacttctccctgaatttgaaataattggaacaacattgacttaaa 1023
QY      1129      gtacgggttaccactcaactatgtcgtgttgtagaggtctc---caaatcaaaaga 1185
Db      1024      gtgagagatcactcctagcaatcactgtatgtcgtgactctctccaatgtgcaaa 1083
QY      1186      caataaagatttgaaactgtgtcgaagatgcaagtcacatcgtcacaaatgactcctg 1245
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QY      1246      atgaacgatgttcaacgtgtgctggttgagtagacatacttgacaacgagatcaaaaa 1305
Db      1144      aagcaaatgcatgagagatgtgctgtgagttacatcactgtccttcacactaaac 1203
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QY      1366      tgaatcatgagatgctgaggggttccctga-----agttgaaatgatttggagag 1419
Db      1264      ttgagttatgagcctgtgagggagatttttgatgagaagaagggaaaaagcatagaagaag 1323
QY      1420      aggttgagaagtgcttgcaagagctgtcgatagatgtctagtcctcgtcgaagaagaa 1479
Db      1324      tggcaacaacatgataaagcgaactatagatagaagcttaatttccatccacaatttca 1383
QY      1480      gtcgagatggaacaaatagatcatgtaaggttcatatcatatataatgacctgtgag 1539
Db      1384      gtttccgttggaacaaatagaag---ttgagaaatgcatgtagtgcacccgtgaactctgt 1440
QY      1540      tgaagaagatcacaaggaggaacatttca 1569
Db      1441      tgaaggagagctcgaaacatgaattttgtga 1470

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RESULT 14  
AAS03717  
ID AAS03717 standard; cDNA; 2880 BP.

AC AAS03717;  
DT 29-AUG-2001 (first entry)  
DE DNA encoding Rx 193, a modified resistance protein.  
XX  
XX Rx; modified resistance; NBS, LRR, cell death; autoactivator;  
KW nucleotide binding site; leucine rich repeat; pathogen resistance;  
XX plant; ss.  
OS Solanum tuberosum.  
XX Synthetic.

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FH      Key      Location/Qualifiers
FT      CDS      37..2850
FT      FT       /tag= a
FT      FT       /product= "Modified resistance protein 193"
PN      WO200129239-A2.
PD      26-APR-2001.
PF      12-OCT-2000; 2000MO-GB03930.
PR      15-OCT-1999; 99GB-0024483.
PA      (PLAN-) PLANT BIOSCIENCE LTD.
PI      Bendahmane A, Baulcombe DC;
XX      WPI, 2001-290924/30.
DR      P-PSDB; AA002147.
XX      Modifying activation characteristics of plant resistance proteins to
PT      produce autoactivator polypeptide capable of activation in absence of
PT      elicitor, by introducing modifications in amino acid sequence of
XX      protein -
XX      Disclosure; Page 46-57; 77pp; English.
XX      The sequence represents the coding sequence of Rx clone 193, a modified
CC      resistance autoactivator. Rx encodes an NBS-LRR polypeptide having a
CC      nucleotide binding site (NBS), leucine rich repeat (LRR), and which
CC      mediates cellular response leading to pathogen resistance and/or cell
CC      death or dysfunction in response to an elicitor. The Rx was modified by
CC      introducing modification to the amino acid sequence to produce an
CC      autoactivator polypeptide, capable of activation in absence of an
CC      elicitor. Decoupling of resistance response from its natural elicitor is
CC      useful for developing novel pathogen resistant plants. The modified
CC      resistance proteins are useful for conferring resistance to non-natural
CC      agents or stimuli and also for investigating resistance response pathways
CC      and protein interactions e.g. with activators and repressors.
XX      Sequence 2880 BP; 864 A; 512 C; 641 G; 863 T; 0 other:
SQ

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Query Match 8.6%; Score 266.4; DB 22; Length 2880;  
Best Local Similarity 54.4%; Pred. No. 8,7e-60;  
Matches 734; Conservative 0; Mismatches 571; Indels 45; Gaps 8;

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QY      292      taagaagaattgcaagtgtcgtggaatatacaatcaactgagactaagcagctgac 351
Db      209      tctgtagagtagatatacaacaacagaagatattgttaccctcggaatcaagaatgtttt 268
QY      352      tgggagaaataaaagccagaanaaaaagcgctgcgaaggttctgccaagcctcgaac 411
Db      269      tagcagaagatttgagagaaagaagaagcaggtcattggtggagatttttctgcctcga 328
QY      412      aagtagcagaagacatggtcatatcttggaaagatgcgcaaaagatccaagaataagaa 471
Db      329      aagcactagaatgcatgtattccacgctgaaacagtgtagtgcaaatcgcaacatgca 388
QY      472      aacaagatcaagaagaatattgttcatgatttccaaagtccaacaacagatatttga 531
Db      389      aagatctaaacacacaactagctcgtgtcagttactcgt---aacatgattgtgagc 445
QY      532      agtttaacacataatggttgacgtgtagatcaagaagaaagaaagttgttagagatctga 591
Db      446      agcccgagagataatattgttgcgttgaaatgaaatgtagatgtagtgcgtgcaacttg 505
QY      592      ctagaagactactctgggaacccaagtcacatccgatttgcggatgggagcatagtga 651

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Db 506 ctgagag---aggaaggaactagaaatgtgtcctcaatcgttaaggatgaggagcatcgga 562  
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 Db 563 aaacacattgataaagaagttatcaatgatcaatcattatgacgtttgatttc 622  
 QY 712 atgctggtgtacatcatctcaacagacacaaagaagaatttgcgtggtcttcgc 771  
 Db 623 gtgcaaaagcaactgtttcaacagagattgtgtgagaatgtactccttagcctcttc 682  
 QY 772 attccacaataaavtgatgacagagttaatgattgttgaagcagagcttagcaaca 831  
 Db 683 cttgacaagtgatgacactgcat-----galtcagctagcggacc 721  
 QY 832 tgttacgaaaagtgttaagaagaagaggtacttaattgtcttgcgttgatgatactgagtt 891  
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 QY 892 gtgagagtgtgagatgagcgttgagacagcttcccaactgaaagacatgacagagagtcgaa 951  
 Db 782 cagaagcttggatgataataaactatgttccagactgttataac---ggaagcagaa 838  
 QY 952 tactgttgaactacccgtaatagatagactgtttatgctggtgtgagaaattttctt 1011  
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## RESULT 15

AAS03719  
 ID AAS03719 standard; CDNA; 2885 BP.  
 XX AAS03719;  
 AC  
 XX

DT 29-AUG-2001 (first entry)  
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 DE DNA encoding Rx 32, a modified resistance protein.  
 XX  
 KW Rx: modified resistance; NBS; LRR; cell death; autoactivator;  
 KW nucleotide binding site; leucine rich repeat; pathogen resistance;  
 KW plant; ss.  
 XX  
 OS Solanum tuberosum.  
 OS synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 37-2850  
 FT /tag= a  
 FT /product= "Modified resistance protein 32"  
 XX  
 W0200129239-A2.  
 PD 26-APR-2001.  
 XX  
 XX 12-OCT-2000; 2000WO-GB03930.  
 PE  
 XX 15-OCT-1999; 99GB-0024483.  
 PR  
 XX (PLAN-) PLANT BIOSCIENCE LTD.  
 PA Bendalmane A, Baulcombe DC;  
 PI  
 XX WPI: 2001-290924/30.  
 DR P-PSDB; AAU02149.  
 XX  
 PT Modifying activation characteristics of plant resistance proteins to  
 PT produce autoactivator polypeptide capable of activation in absence of  
 PT elicitor, by introducing modifications in amino acid sequence of  
 PT protein -  
 XX  
 PS Disclosure: Page 46-57; 77pp; English.  
 XX  
 CC The sequence represents the coding sequence of Rx clone 32, a modified  
 CC resistance autoactivator. Rx encodes an NBS-LRR polypeptide having a  
 CC nucleotide binding site (NBS), leucine rich repeat (LRR), and which  
 CC mediates cellular response leading to pathogen resistance and/or cell  
 CC death or dysfunction in response to an elicitor. The Rx was modified by  
 CC introducing modification to the amino acid sequence to produce an  
 CC autoactivator polypeptide, capable of activation in absence of an  
 CC elicitor. Decoupling of resistance response from its natural elicitor is  
 CC useful for developing novel pathogen resistant plants. The modified  
 CC resistance proteins are useful for conferring resistance to non-natural  
 CC agents or stimuli and also for investigating resistance response pathways  
 CC and protein interactions e.g. with activators and repressors.  
 CC  
 XX Sequence 2885 BP; 861 A; 514 C; 649 G; 861 T; 0 other;  
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## OM nucleic - nucleic search, using sw model

Run on: September 11, 2002, 11:42:09 ; Search time 10435.2 Seconds  
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6214.659 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

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2: gb\_htg:\*  
3: gb\_in:\*  
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6: gb\_pat:\*  
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9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
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25: em\_pl:\*  
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27: em\_sts:\*  
28: em\_un:\*  
29: em\_vi:\*  
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31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htg\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No. Query Match Length DB ID Description

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DEFINITION Sequence 2 from Patent WO0107635.  
ACCESSION AX076881  
VERSION AX076881.1 GI:13121542  
KEYWORDS  
SOURCE  
ORGANISM Capsicum annuum.

REFERENCE  
AUTHORS Staskiewicz, B.J., Dahlbeck, D. and Tai, T.H.  
TITLE Bs2 resistance gene  
JOURNAL Patent: WO 0107635-A 2 01-FEB-2001;  
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)  
FEATURES  
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Location/Qualifiers  
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 Expression of the Bs2 pepper gene confers resistance to bacterial  
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 Proc. Natl. Acad. Sci. U.S.A. 96 (24), 14153-14158 (1999)  
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VERSION AX076883.1 GI:13121544  
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 REFERENCE 1 (bases 1 to 2718)  
 AUTHORS Staskiewicz, B. J., Dahlbeck, D. and Tai, T. H.  
 TITLE Bz2 resistance gene  
 JOURNAL Patent: WO 01/635-A 4 01-FEB-2001;  
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REFERENCE  
 1 (bases 1 to 3254)  
 AUTHORS Bendahmane, A., Querci, M., Kanayka, K. and Paulcombe, D.C.  
 TITLE Agrobacterium transient expression system as a tool for the isolation of disease resistance genes: application to the Rx2 locus in potato  
 JOURNAL Plant J. 21 (1), 73-81 (2000)  
 MEDLINE 20117531  
 REFERENCE 2 (bases 1 to 3254)  
 AUTHORS Bendahmane, A.  
 TITLE Direct Submission  
 JOURNAL Submitted (13-SEP-1999) Bendahmane A., Sainsbury Laboratory, John Innes Center, Colney Lane, Norwich NR4 7UH, UNITED KINGDOM  
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LOCUS Sequence 20 from Patent WO0129239.  
DEFINITION AX133916  
ACCESSION AX133916  
VERSION AX133916.1 GI:14139868  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct.  
REFERENCE  
1 (bases 1 to 3683)  
AUTHORS Bendallman, A. I. and Baulcombe, D. C.  
TITLE Modified resistance genes  
JOURNAL Patent: WO 0129239-A 20 26-APR-2001;  
Plant Bioscience Limited (GB)  
FEATURES  
location/Qualifiers  
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ORIGIN

Query Match 8.8%; Score 272.8; DB 6; Length 3683;  
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Matches 738; Conservative 0; Mismatches 567; Indels 45; Gaps 8;

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RESULT 8  
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LOCUS AF195939 10331 bp DNA linear PLN 31-Oct-1999  
 DEFINITION Solanum tuberosum disease resistance protein Gpa2 gene, complete cds.  
 ACCESSION AF195939  
 VERSION AF195939.1 GI:6164968  
 KEYWORDS  
 SOURCE potato.  
 ORGANISM Solanum tuberosum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.  
 REFERENCE 1 (bases 1 to 10331)  
 AUTHORS Van der Vossen, E.A.G.  
 TITLE Direct Submission  
 JOURNAL Submitted (19-Oct-1999) Genomics, CPRO, Droeveendaalsesteeg 1, Wageningen 6708 PB, The Netherlands  
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 Best Local Similarity 54.7%; Pred. No. 1,2e-51;  
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Db	5228	AAGATCTRAAACCCAAACTAGCTCACTTGTCAAGTTACTGTAAC---ATGATGTTGAC	5285
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OY	712	atgcctgggtactacatatctccaacgacacaaagaagaatttgcctgggctctgc	771
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LOCUS	AF265664	187352 bp	DNA linear
DEFINITION	Solanum tuberosum resistance gene cluster, complete sequence.		
ACCESSION	AF265664		
VERSION	AF265664.1	GI:9587171	
KEYWORDS			
SOURCE	potato.		
ORGANISM	Solanum tuberosum		
REFERENCE	Euraivola, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.		
AUTHORS	1 (bases 1 to 187352)		
TITLE	van der Vossen, E.A.G., Rouppé van der Voort, J., Kanyuka, K., Bendahmane, A., Sandbrink, D.M., Baulcombe, D., Bakker, D., Stiekema, W.J., and Klein-Lankhorst, R.		
JOURNAL	Homologs of a single resistance gene cluster of potato confer resistance to distinct pathogens: a virus and a nematode		
REFERENCE	Plant J. (2000). In press		
AUTHORS	2 (bases 1 to 187352)		
TITLE	van der Vossen, E.A.G., Rouppé van der Voort, J., Kanyuka, K., Bendahmane, A., Sandbrink, D.M., Baulcombe, D., Bakker, D., Stiekema, W.J., and Klein-Lankhorst, R.		
JOURNAL	Direct Submission		
FEATURES	Submitted (10-MAY-2000) Genomics, Plant Res. Int., Drenvendaalsteeg 1, Wageningen, Gld 6708PB, Netherlands		
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RESULT 10
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DEFINITION Sequence 12 from Patent WO954490.
ACCESSION AX012617
VERSION AX012617.1 GI:9998601
KEYWORDS potato.
SOURCE Solanum tuberosum

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Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

REFERENCE
1 (bases 1 to 3229)
AUTHORS Baulcombe, D.C., Bendahmane, A. and Kanyuka, K.V.
TITLE Plant-derived resistance gene
JOURNAL Patent: WO 9954490-A 12 28-OCT-1999;
BAILCOMBE DAVID CHARLES (GB); BENDAHMANE ABDELHAFID (GB); KANYUKA
KONSTANTIN VALERIEVICH (GB); PLANT BIOSCIENCE LIMITED (GB)

FEATURES
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Best Local Similarity 55.0%; Pred. No. 1.7e-51;
Matches 728; Conservative 0; Mismatches 551; Indels 45; Gaps 8;

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 DEFINITION Sequence 13 from Patent WO954490.  
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 ORGANISM Solanum tuberosum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum.  
 REFERENCE 1 (bases 1 to 3229)  
 AUTHORS Baulcombe, D.C., Bendahmane, A. and Kanyuka, K.V.  
 TITLE Plant-derived resistance gene  
 JOURNAL Patent: WO 954490-A 13 28-OCT-1999;  
 BAUDCOMBE DAVID CHARLES (GB); BENDAHMANE ABDELHAFID (GB); KANYUKA  
 KONSTANTIN VALERIEVICH (GB); PLANT BIOSCIENCE LIMITED (GB)  
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 ORIGIN

Query Match 8.8%; Score 272.4; DB 6; Length 3229;  
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ACCESSION	AX012614		
VERSION	AX012614.1		
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SOURCE	potato.		
REFERENCE	Solanum tuberosum		
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
TITLE	Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots;		
JOURNAL	Asteridae; euastrerids I; Solanales; Solanaceae; Solanum.		
FEATURES	1 (bases 1 to 3220)		
SOURCE	Baulcombe, D.C., Bendahmane, A. and Kanyuka, K.V.		
REFERENCE	Plant-derived resistance gene		
JOURNAL	Patent: WO 9954490-A 9 28-OCT-1999;		
FEATURES	BALCOMBE DAVID CHARLES (GB); BENDAHMANE ABDELHAFID (GB); KANYUKA		
SOURCE	KONSTANTIN VALENTIEVICH (GB); PLANT BIOSCIENCE LIMITED (GB)		
LOCATION/Qualifiers	1..3220		
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	SOURCE	potato.			
	ORGANISM	Solanum tuberosum			
	REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.			
	AUTHORS	1 (bases 1 to 18284)			
	TITLE	Bendahmane,A., Kanyuka,K. and Baulcombe,D.C. The Rx gene from potato controls separate virus resistance and cell death responses			
JOURNAL	MEDLINE	Plant Cell 11 (5), 781-792 (1999)			
REFERENCE		99264301			
AUTHORS		2 (bases 1 to 18284)			
TITLE		Bendahmane,A.			
JOURNAL		Direct Submission Submitted (03-AUG-1998) Bendahmane A., The Sainsbury Laboratory, John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7QH, United Kingdom			
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GenCore version 4.5  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
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#### SUMMARIES

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#### ALIGNMENTS

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; Sequence 4, Application US/09360186
; Patent No. 6262343
; GENERAL INFORMATION:
; APPLICANT: Staskawicz, et al.
; TITLE OF INVENTION: B2 Resistance Gene
; FILE REFERENCE: 50687
; CURRENT APPLICATION NUMBER: US/09/360,186
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: 60/093,957
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2718
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; Patent No. 6262343  
; GENERAL INFORMATION:  
; APPLICANT: Staskawicz, et al.  
; TITLE OF INVENTION: B2 Resistance Gene  
; FILE REFERENCE: 50687  
; CURRENT APPLICATION NUMBER: US/09/360,186  
; EARLIER FILING DATE: 1999-07-23  
; EARLIER APPLICATION NUMBER: 60/093,957  
; NUMBER OF SEQ ID NOS: 9  
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; TYPE: DNA  
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; NAME/KEY: CDS  
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US-09-360-186-2

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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2718; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 993 ggtgtgagaagattttctctgtcgatagcttcaatgatacagaatgttgaggtctc 1052  
QY 961 ttcaaaaagtgcagcattttcaagtgaagcattacacatagatgtcgaactgttgaag 1020  
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RESULT 4  
US-08-680-327-1

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Sequence 1, Application US/08680327
Patent No. 5859321
GENERAL INFORMATION:
APPLICANT: Staskawicz, Brian S., Oldroyd, Giles Edward,
APPLICANT: Salmeron, John M., Rommens, Catus
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PLANT
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klarguist Sparkman Campbell Leigh &
ADDRESSEE: Winston
STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
STREET: Suite 1600
City: Portland
STATE: Oregon
COUNTRY: United States of America
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/680,327
FILING DATE: July 11, 1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/310,912
FILING DATE: September 22, 1994
CLASSIFICATION: 800
APPLICATION NUMBER: 08/227,360
FILING DATE: April 13, 1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Alan E.
REGISTRATION NUMBER: 35,123
REFERENCE/DOCKET NUMBER: 5151-45038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5475 base pairs
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
US-08-680-327-1

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Query Match          6.3%; Score 172.2; DB 2; Length 5475;
Best Local Similarity 50.6%; Pred. No. 2e-39;
Matches 554; Conservative 0; Mismatches 523; Indels 18; Gaps 5;

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QY 476 ggaacagtgtagaagatctgactagaagctactctggggaacccaagtctccga 535
DB 3302 TAGATGAATTAAAGATTAAGTACTTGGAGGATACCT---GAGCTTGATGTCATCTCA 3358
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DB 3359 TCGTTGGATGCCAGAGATTGGCAAGACTACACAGCAAGAAAGATTACAAATGATCCAG 3418
QY 596 caattctatgcggtttgtagtgcctgacgtggtggtctaccatactcaacagcacaca 655
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DB 4310 GTGGAGAGGTGTAT 4324

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RESULT 5
US-09-228-246-3
Sequence 3, Application US/09228246
Patent No. 6245510
GENERAL INFORMATION:
APPLICANT: Staskawicz, B. S. et al.
TITLE OF INVENTION: PRE Protein and Nucleic Acid Sequences: Compositions
TITLE OF INVENTION: and Methods for Plant Pathogen Resistance
FILE REFERENCE: 51700
CURRENT APPLICATION NUMBER: US/09/228,246
CURRENT FILING DATE: 1999-01-11
EARLIER APPLICATION NUMBER: 08/680,327
EARLIER FILING DATE: 1996-07-11
EARLIER APPLICATION NUMBER: 08/310,912
EARLIER FILING DATE: 1994-09-22

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; EARLIER APPLICATION NUMBER: 08/227,360  
 ; EARLIER FILING DATE: 1994-04-13  
 ; NUMBER OF SEQ ID NOS: 5  
 ; SOFTWARE: Patentln Ver. 2.0  
 ; SEQ ID NO 3  
 ; LENGTH: 5475  
 ; TYPE: DNA  
 ; ORGANISM: Lycopersicon esculentum  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(5475)  
 US-09-228-246-3

Query Match 6.3%; Score 172.2; DB 4; Length 5475;  
 Best Local Similarity 50.6%; Pred. No. 2e-39;  
 Matches 554; Conservative 0; Mismatches 523; Indels 18; Gaps 5;

QY 416 caagttcaacaacagatatttgaaaggttaagacaataatgttgagcgtgatgaca 475  
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 QY 536 ttgtggagtgaggagcagataggtaaacacttagcaagaagttaacatgatgaat 595  
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# RESULT 6

US-08-680-327-2  
 ; Sequence 2, Application US/08680327

; Patent No. 5859321

## GENERAL INFORMATION:

APPLICANT: Staskawicz, Brian S., Oldroyd, Giles Edward,  
 APPLICANT: Salmeron, John M., Rommens, Caus  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PLANT  
 TITLE OF INVENTION: PATHOGEN RESISTANCE  
 NUMBER OF SEQUENCES: 15  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Klarquist Sparkman Campbell Leigh &  
 ADDRESSEE: Whinston  
 STREET: One World Trade Center  
 STREET: 121 S.W. Salmon Street  
 STREET: Suite 1600  
 CITY: Portland  
 STATE: Oregon  
 COUNTRY: United States of America

ZIP: 97204  
 COUNTRY: United States of America

## COMPUTER READABLE FORM:

MEDIUM TYPE: Disk, 3-1/2 inch  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: MS DOS  
 SOFTWARE: Wordperfect 5.1

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/680,327  
 FILING DATE: July 11, 1996  
 CLASSIFICATION: 800

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/310,912  
 FILING DATE: September 22, 1994  
 CLASSIFICATION: 800  
 APPLICATION NUMBER: 08/227,360  
 FILING DATE: April 13, 1994  
 CLASSIFICATION: 800

## ATTORNEY/AGENT INFORMATION:

NAME: Dow, Alan. E.  
 REGISTRATION NUMBER: 35,123  
 REFERENCE/DOCKET NUMBER: 5151-45038  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (503) 226-7391  
 TELEFAX: (503) 228-9446

## INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 10968 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double stranded  
 TOPOLOGY: linear  
 US-08-680-327-2





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QY 1016 gaaagcaaatcgagatgtagatgcaggtttaccactaatctatgtcgtgtgttcagggc 1075
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Db 7711 gatttgaataatcaaaaagtcttagagaggttgcctctcctcagttgttagtagctgtg 7770
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1076 ttctcaaatctaaagaacatagaagattggaacactgttgcataagatgtaagtcatt 1135
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 7771 ttctgaaacaagaagaagaagacactagattcatcagaagaagttagagaacaagcttaagt 7830
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1136 tgcacaacatgactctgtgaacagatgttcacgtgtgtgtgtgtgtgtgtgtgtgtgt 1195
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 7831 ccagagagattgagcagcttggaagagagcatatctataattgattcagttacaagaatt 7890
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1196 tgacaagcagatctaaacatgtctctcatttgcatttgcgaattttccagaagacagtgata 1255
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 7891 taccacacatcttaagccttgccttctcatttgcgaagattttgcagggaaagagata 7950
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1256 ttccagtgagaatttgatgagatcatgagtgctgaggggttctc-----gaagttgg 1309
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 7951 ttcatgtctcaaaaatgaccagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 8010
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1310 aaaaatgttggaagagagaggtgtggaagatgtgttcgaagagctgttcgataagatgtcag 1369
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 8011 aaaaagacaagaagaatcaccgacaggttcttgacgactcttattgttgaagatgtgag 8070
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1370 tctcgtgcagcagaagatgagatgcagtggaacaaaatgatcatgttaagttcagtcagc 1429
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Db 8071 tgatggcccttgaggaagagacctaact--acaaagtgaaaacgtgcgcattcatcagatt 8127
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1430 taataatgacctgtgcgtgagagaagatccaagagagaacatttattcatgaagacaca 1489
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 8128 tgttgataaatcttgcatgagaaagccaaaagaagagatttctctcccaaatcaata 8187
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RESULT 8
US-08-310-912A-157
; Sequence 157, Application US/08310912A
; Patent No. 5981730
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas F.
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND DETECTION
; NUMBER OF SEQUENCES: 208
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2904
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/310,912A
; FILING DATE: September 22, 1994
; CLASSIFICATION: 536

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/227,360
; FILING DATE: April 13, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lech, Karen F.
; REGISTRATION NUMBER: 35,238
; REFERENCE/DOCKET NUMBER: 00786/254001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 100254
; INFORMATION FOR SEQ ID NO: 157:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5134 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-310-912A-157

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Query Match 6.0%; Score 164.2; DB 2; Length 5134;
Best Local Similarity 50.3%; Pred. No. 4e-37;
Matches 544; Conservative 0; Mismatches 518; Indels 19; Gaps 5;

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QY 416 caagttcaacaacagatatttgaagttagaacaataatggttgagcgtgatgataaa 475
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1196 CATCTTTTACGCTTACTCAAAAGACCAAGCAAGAAATGAGAGGTTTCAGAGATCAAA 1255
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 476 ggaacaagttgttagaagatctactagaagctactctgagggaacccaagatcccca 535
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1256 TAGATGATTAAGAGATTAACCTACTTGAGAGATCACT--GAGCTTGATGATCAATCCAA 1312
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 536 ttgtcggatggagagacatagtgtaaaacaaccttagcaaaagaagttacaatgtgaat 595
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1313 TCGTTGGCAGCCAGGATTTGGCGAAGACTACACTAGCAAGAAAGATTTACAAATGATCCAG 1372
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 596 caattctatgcgctttgatgattcattcagctcgtggtcaccatctcaacagcacacaaca 655
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1373 AAGTCACCTCTCGCTTCGATGATGCTCAATGCTCAATGCTGTGATCACTCAATTTATTCATGCA 1432
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 656 aggaatattgtcgtggcctctctgcatccacaatcgaatgagatgaggttaagatga 715
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1433 GAGAGTTGTTGTCACCATTTTGAATGATGTGCTTGAGCTTGCATGCCAATGAAGAAA- 1491
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 716 ttgttgaagcagctagcagacatgtttacagaagaagtttaagagagaaggtacttaa 775
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1492 --GAAGATGAGAAATAGCTGATGATCTACGCCGATTTTGTGACCAAGAGATTCCTTGA 1549
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 776 ttgtcttgatgatatctgagatgttgaagtgtgggataggcgtggagacgattgttccaa 835
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1550 TTCTCATTTGATGTGTGTGGGACTATTAAGTGTGGGCAATCTATGATATGCTT---CA 1606
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 836 ctgaagacaaatgcaggaagtcgaatactgttgaactccgtaalgtatgaatgagctgtgt 895
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1607 GTGATGTTTCAATAGAGAGTAGAATATATCTTACCAACCCGCTTGAATGATGTGGCGAAT 1666
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 896 atgctgtgtgagaatttcttcttgcgagatgttcagatgaagatgaagatgttga 955
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1667 AATGCAAAATGTGAAGTGAATGCCCATCATCTTGTATTATCAGAGATGAGCAAGATTTGA 1726
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 956 gtcttcaaaatgtagcagcttctcaagtgaagcattacataatgattgagagctgtg 1015
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1727 CATTATTACAGAAAGAGCTTTTCAAGGAGAGAGCTGTCCACTGCAACTTGAAGATGTGG 1786
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1016 gaaagcaaatcgagatgtagatgcagcgtttaccactaatctatgtcgtgtgttcagggc 1075
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1787 GATTGGAATATCAAAAAGCTTGTAGAGGGTGTGCTCTCCTCAGTTGTGTAGTGTGCTG 1846
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1076 ttctcaaatcaaaagaagacatgaagatgtgaaactgtgtcgttaagaatgtcaagtcatt 1135
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1847 TTCTGAAACGAAAAAGAGACACTAGATTTCATGGAAGTAGAACAAGTCTAAGTT 1906
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Qy	1136	tcgtccacaatgatcctcgatgaaacgcatgtgtcactcgtcttggttggttgatcagatcaact	1195
Db	1907	CCGAGAGGATTTGGCAGCTTGGAGAGAGAGGATATCTATAATTGGATTTCAGTTACAGAAATT	1966
Qy	1196	tgaacagcgatctcaaaaacatgccttcctgcatttcgaaattcttcocgaagacagtgta	1255
Db	1967	TACCAACCTATCTTAAAGCCTTGTTTCTCTATTTTTGGAGATTTTTTGCAGGGAAGGATA	2026
Qy	1256	ttccagtgaaagaaattgatgagatcagatgagctgtaggggttccctgaaagtgtgnaaag	1315
Db	2027	TTCTATGACTCAAAAATGACCAAGTTGTGGGTAGTCGAAGTTGTACAAAGCAAAACMG	2086
Qy	1316	atttggaagagagaggtt-----gagaagtggtttgcaagagctgtcogatagatgctta	1368
Db	2087	AAAAGGACACAGAGATGCCGCACAGAGTTCCTTGGAGATCTTATTTGGTAGAATGTG	2146
Qy	1369	gtctcgtctcagcaagaaagctcgatgtagatggaacaaaattagatcagtgaagttcatgat	1428
Db	2147	GTGATGGCCATGNGAGAGAACCTAATG---CCAGGTAAAACTGCCCATTTTCATGAT	2203
Qy	1429	ctaatatatacctctgctgtagagagaagttcaaaaggggaaacattttatcatgaagac	1488
Db	2204	TTGTTCATTAATTCCTCATGCAAAAGGCCAAACAAGAGGATTTCTCTCCATCATCAAT	2263
Qy	1489	a 1489	
Db	2264	A 2264	

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RESULT      9
US-09-301-085-157
; Sequence 157, Application US/09301085
; Patent No. 6262248
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumitaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindinos, Michael N.
; APPLICANT: Yu, Guo-liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
; TITLE OF INVENTION: DETECTION METHODS
; FILE REFERENCE: 00786/254002
; CURRENT APPLICATION NUMBER: US/09/301,085
; CURRENT FILING DATE: 1999-04-28
; EARLIER APPLICATION NUMBER: 08/310,912
; EARLIER FILING DATE: 1994-09-22
; EARLIER APPLICATION NUMBER: 08/227,360
; EARLIER FILING DATE: 1994-04-13
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 157
; LENGTH: 5134
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-301-085-157

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Query Match	6.08;	Score 164.2;	DB 4;	Length 5134;
Best Local Similarity	50.38;	Pred. No. 4e-37;		
Matches 544; Conservative	0;	Mismatches 518;	Indels 19;	Gaps 5;

Qy	416	caatttcaacaacagatatttgaagttaagaaacatatgtttgaagttgatacaaa	475
Db	1196	catcttttcgccttaactcaacaaagcaaaagaaatgtgaaggttttcagataaaa	1255
Qy	476	ggaacacgtttgtgaagatctgactagaagctactcttggggaaaccacaagtcacccgga	535
Db	1256	tagattgatttaagataactactcttggaaagatcacct--tagcttggatctatctctaa	1312
Qy	536	tttgcggatgtggggacatgtgtcaaaacaaccttgcacaaagaatttcaatgtatgat	595

Db	1313	tcgtttgcacgcccaggaatttggcagaagacatacactcagcaaaagaaagtattcaatctgacg	1372
QY	596	caattctaagccglttttgatgtlctacgtcctggctacacatctcaacagcaacaacaa	655
Db	1373	aagtcacctctcgcttcgatagtctacgtcccaatgltgttgactcaatataattatgga	1432
QY	656	aggaatttggcttgggcctctctgcataccaatcaacaatgagatgaacgggttaagaga	715
Db	1433	gagagctgtgtlccacacatttgaagatgtcttgagcttcctctgatacgaatgaanaa	1491
QY	716	ttgttgaagcagagctagcagacatgtltaacagaanaagtttaagaagaaagagtaactaa	775
Db	1492	--ggaagtgaagaaatagatcgatctacgacccgagattttgttggccaagagatcttga	1549
QY	776	ttgtcttgatgatatacttggaattgttgaagtgtgggaatggcgttgagacgaatgcttcaa	835
Db	1550	ttccattgatgatagtgttgggaactataaagtgtgggagacaactaagtatgtctt--ca	1606
QY	836	ctgaaagcaatgvcagcgagtcggaatactgttgaactcccgtaagttaagatagcttgt	895
Db	1607	gtgatagttccaataagagaaagataagatatcctaacaacccgcttgaaatgatagtgcgcgat	1666
QY	896	atgctgtgtgtagaagaattttctcttgcgatagaagcttcaatgataagaatgagatgga	955
Db	1667	atgccaatgtgaagaatgataccccaatcatcttcgttattcagaagatgacgagagttgga	1726
QY	956	gtctttccaagaagcgagcttttcaagtgaaagcatctaccataagatgttcggaactgtg	1015
Db	1727	catattacagaanaagagcttcttccaagaaagaaagagctgtccaccctgaacttgaagatggg	1766
QY	1016	gaaagcaaatgcagatcgtgaatgttcaacgggttcaacatactatcttgcgtgttgaagggc	1079
Db	1787	gatttgaataatcaaaaagttgtagaggggtgtgcctctcagttgtgtatgaagctgtg	1846
QY	1076	tttccaatctcaaaaagaaataatgaagatgtggaatactgttctaagaatgtcaagtcata	1135
Db	1847	ttcttgaacaacagaanaaagaaagacactagatcatctgaaagatgaatgaacaagaactaagt	1906
QY	1136	tcgttcaacaatgatacttcgtgaacgagatgttcaacggttgcgttggttgaatctacgtact	1195
Db	1907	ccccagagatgtgacgtcttgaaagagagacatactataatttgatattcagttacaagaatt	1966
QY	1196	tgaacaagcagatcaaaaaacatgtctcttcgtcatttcggaaattttccaagaagcagtata	1255
Db	1967	taccacacatcttaagccttgttcttctcatttttgaaagatttttgcaggggaaagagata	2026
QY	1256	ttccaagtgaagaattttgatgatacatgagatgtgcataagggttccctgaagtttgaanaatg	1315
Db	2027	ttcatgactcaaaaatgacaagaattgttgggtagctgaanaagttgttatacagaacaacaag	2066
QY	1316	atttggaaagagaggtt-----gagaagttgttgcagaagcctgtgcgatatgtctta	1368
Db	2087	aaaagagcagaagaagataccgcgacaagaagtttctcttgacgactatattgttggagaactg	2146
QY	1369	gttcctgttcagcaagagaaagtgtgagtgtgagacaanaattagatcatgtaagttcaatgat	1428
Db	2147	gttgaagccacatgagagaagaacttaag---ccaaggtgtaaaacgtgtccgcatccaatgat	2203
QY	1429	ctaatatatagcctgttgcgtgagagaagttccaaggtgaanaaatlttatactgaagac	1488
Db	2204	ttgttgcataaattctgtcatgtaagaagccaacaagaagagatttctcttccagatcaat	2263
QY	1489	a 1489	
Db	2264	a 2264	

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RESULT 10
PCT-US95-04589-157
; Sequence 157, Application PC/TUS9504589
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.

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[illegible]

OY	776	ttcttcgtgagatcctggaagttgaaagtgcggagatgcgctgaaacagatcttccaa	835
Db	1550	TTTCATTTGATGANGTGTGGGACTATTAAGTGTGGACATCTATGTATGTCTT---CA	1606
OY	836	ctgaagaacatgcgagagtcgatactgtgtactaccgtaatgaatgaagtcgtgt	895
Db	1607	GTGATGTTCCTCAAAATAGGAGTGAATTAATCTCAACAACCGCTGAATGATGTGCCGAAT	1666
OY	896	atgctgtgtgtagagaattttcttttcgcgatagccttcatlgtatgcataagaatgaaatgga	955
Db	1667	ATGTCAAAATGTGAAGATGATCCCATCATCTCTTGTTTATTCAGAGATGACGAGATCTTGA	1726
OY	956	gtctcttcaaaagcgacgaatttccaagtgaagcatctaacatctgaattcgatgcagatctgtc	1015
Db	1727	CATTATTACAGAAAGAGTCTTTCCAAAGAGAGCTGTCTCACCCTGAACCTTGAAAGATGTGG	1786
OY	1016	gaaagcaaatcgcagatgaaatgtcacggygttaccatactatgtcgtgtgttcagaggc	1075
Db	1787	GATTGTGAATPTCAAAAAGTTGTAGAGGGTGGCTCTCACTTGTGTTAGTACGTGGTG	1846
OY	1076	tttccaatctaaagagacatagaagatttggaaaactgttgcataagatgttcaagtcact	1133
Db	1847	TTTGAAACAGAAAAAGACACACTGATTCATGAAAGTACTAGAAACAAAGCTTAAGTT	1906
OY	1136	tcgtcaacaatgatccctgatacgaatgttcaacgtgttcaacgtgtgtgtgtgaattacgaact	1195
Db	1907	CCCAAGAGGATTTGCGACTTGTGGAAGAGACATCTATTAATTGGATTCACTTACAAAGATT	1966
OY	1196	tgaacaagcatctaaaaacatctgtctcttcgacttcgaaattttccagaagacagatga	1255
Db	1967	TACCACTACTATCTTAACCTTGTGTTTCTCATTTTGGAGATTTTGGACAGGAAGGATTA	2026
OY	1256	ttcagaatgaagaattgaatgaatcatgatacgtatgcgtgaaggttccctgaagtgtgaanaatg	1315
Db	2027	TTTCATGACTCAAAANATGACCAAGTTGTGGTACTGTAAAGATTGTACAGCAACAACAG	2086
OY	1316	atttgaagagagagatgt-----gagaagtgttttccaagagctgttcgataagatgtcta	1368
Db	2087	AAAAAGACAAAGAGATGACCCGACAAAGTTTCTTGAGCATCTTAATTGGTGAACATCTG	2146
OY	1369	gtctcgttcgcaagaagaagtgcagatgatacaaaaaaattagatcatgtlaagttcatgat	1428
Db	2147	GTGATGTGCCATGGAGAAAGACACCTAATG---CCAAAGTCAAAAACGTCCGCAATTCAT	2203
OY	1429	ctaatactaacctgtgcgtgagagagaagttcaaaagggagaacattttatcatgtagacac	1488
Db	2204	TTGTTGCAATTAATTTCTGCATGAAAGGCCAAACAAAGAGGATTTCTTCTCCAGATCAAT	2263
OY	1489	a	1489
Db	2264	A	2264
RESULT 11			
US-08-947-823-2			
Sequence 2, Application US/08947823			
Patent No. 6114605			
GENERAL INFORMATION:			
APPLICANT: Williamson, Valerie M.			
APPLICANT: Kaloshian, Isgouhi			
APPLICANT: Yaghoobi, Jafar			
APPLICANT: Bodeau, John			
APPLICANT: Milligan, Stephen			
TITLE OF INVENTION: Procedures and Materials for Confering			
TITLE OF INVENTION: Pest Resistance in Plants			
NUMBER OF SEQUENCES: 5			
CORRESPONDENCE ADDRESSES:			
ADDRESSEE: Townsend and Townsend and Crew LLP			
STREET: Two Embarcadero Center, Eighth Floor			
City: San Francisco			
STATE: California			
COUNTRY: USA			

```

ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/947,823
FILING DATE: 09-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/18802
FILING DATE: 09-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,191
FILING DATE: 10-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-070210US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3997 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 85..3852
OTHER INFORMATION: /note="Copy 1 cDNA for M1 nematode"
OTHER INFORMATION: resistance gene of tomato"
US-08-947-823-2

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Query Match 5.5% Score 149.2; DB 3; Length 3997;
Best Local Similarity 49.5%; Pred. No. 7.1e-33;
Matches 512; Conservative 0; Mismatches 498; Indels 24; Gaps 4;

QY 449 acaatagtggtgacgctgcatgatcaagaagaacagctgttgaaagatctgtagaagct 508
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1637 ATAAATATACGTGATGTTTGAGAGAGAACAACTTGATTAAGAAAGCTCACCGTG 1696

QY 509 actctggggaacccaagatcccgatgttcggatggagagagatggttaaaaaacct 568
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1697 GATCGGCGATCTGATGCTCTTTTCGATCACTGGATGCCGGGTTCAAGTAAACTACTT 1756

QY 569 tagcaaaagaagttacaatgatcaatctatgcgcttggatgctcattccctggg 628
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1757 TGGCATACAAAGTATACATATATAGTCAGTTCAGCCGTTTGACCTCGTGCATAGGT 1816

QY 629 ctacatatctcaacagacacaacaaagaagaatttgcctgggaccttcgcatccaca 688
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1817 GCACGCTGCACCAAGATGTGATGAGAAGAGTGTGTAATCAATTTTCAGTCAACTTA 1876

QY 689 tcaaatgatgacaaggttaagatgttggtaagaagagctgacagacatgtaaga 748
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1877 GTGACTCAGAT-----TCAAAATTTGAGTGAGAAATATTGATGTTGCTGATRAAATTA 1930

QY 749 aaagttaaaagaagaagagacttaattgtctgtgataatcctggaagtgtaagtg 808
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DB 1931 AAACAACGTTTGGAAAGAGGATCTTAATTCCTTAGATGAGCTGTGGGATCTACTACAT 1990

QY 809 gggatgacgtgagacgactgttccaactgaagaacatgcaaggagtcgaactgttga 868
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DB 1991 GGGATGAGTAAACAAGACCTTTTC---CTGAATCTAAGAAAGGAAGTAGAGATTATTGGA 2047

QY 869 ctaccggaatgatgaagtagctgtgtagtgtagaagaatttcttcgagatga 928
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DB 2048 CAACCTGGGAAAAGAGAGTGGCTTTGCAATGGAAGCTGAACACTGATCCTTTCACCTTC 2107

QY 929 gcttcatgatcaagaatgagatgagctgttcttccaagaagtcgaacatcttcaagtga 988
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DB 2108 GATTCCTAAGACCAAGATGAAGATTTGGACACTTATAGAAAAAGGCAATTTGGGATGAGA 2167

QY 989 catcacatgatgctcagacgtgttgaaagcaaatcgcagatgaatgcaaggtttac 1048
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DB 2168 GTTGCCCTGATGAAGTATAGATGTCGGTAAAGAAATAGCCGAAATGTGAAGGGCTTC 2227

QY 1049 caactaatgtcgtgtgttgcaaggtcttccaatctcaaaagagcaatgaagaattga 1108
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DB 2228 CTTTGGTGCTGATCTGATTTGCTGAGATCATTCGTGGAAGGAAAAAGAGAGTGTGT 2287

QY 1109 aaactgttgtaagatgtaagatcattcgtacaaatgatccatgataagcagatgta 1168
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DB 2288 GCCTTGAGATTAAGATGATTTGAGTCTCTTTATTTTGAACAGTCAAGTGAAGTGAAGA 2347

QY 1169 gctgcttggttggttgtaagatcagatcctgaaagcgaatcctaaacatgcttgcac 1228
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2348 AAGTATAGAAATTAAGTTATGACATTTACACATCACCTCAAGCCATGCTTGTGTATTT 2407

QY 1229 tgggaattttccagaagacagtgataltccagtgagaatttgatgatacagatgag 1288
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DB 2408 TTGCAAGTTTTCGAAGGACACTTCATTCACATCTATGAGTTGAATGTTATTTTCGCTG 2467

QY 1289 ctgaggggttctct-----gaagttgaaatgatgttgaaaggaggttgagaagtg 1342
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DB 2468 CTGAAGATTTTGTGGAAAGACGAGATGACAGATATGGAAGAGTGTGAAGATTTATA 2527

QY 1343 tgcnaagactgtcgatagatgtctagtcctcgtcgaagcagaagaagtcgagatgaga 1402
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DB 2528 TGGATGATTTTAATTTACACTGCTGTAATTTGTTTCAMTAGATGAGTTAGTACATGCA 2587

QY 1403 aaatgatcatgtaagctcagatcgaataataatgacctgtgctgagagaagttcaaa 1462
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DB 2588 A-----TTTCCAATTCATGATCTTGTGCATGACTTTTGTGTGATTAAGCAAGAA 2638

QY 1463 gggagacaatttt 1476
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DB 2639 AGCAAAATTTGTTT 2652

RESULT 12
US-08-947-823-1
Sequence 1, Application US/08947823
Patent No. 6114605
GENERAL INFORMATION:
APPLICANT: Williamson, Valerie M.
APPLICANT: Kaloshian, Isouhi
APPLICANT: Yaghoobi, Jafar
APPLICANT: Bodeau, John
TITLE OF INVENTION: Procedures and Materials for Confering
NUMBER OF INVENTIONS: Pest Resistance in Plants
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/947,823
FILING DATE: 09-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/18802

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1      FILING DATE: 09-OCT-1997
2      PRIOR APPLICATION DATA:
3      APPLICATION NUMBER: US 60/028,191
4      FILING DATE: 10-OCT-1996
5      ATTORNEY/AGENT INFORMATION:
6      NAME: Bastian, Kevin L.
7      REGISTRATION NUMBER: 34,774
8      REFERENCE/DOCKET NUMBER: 023070-070210US
9      TELECOMMUNICATION INFORMATION:
10     TELEPHONE: (415) 576-0200
11     TELEFAX: (415) 576-0300
12     INFORMATION FOR SEQ. ID NO. 1:
13     SEQUENCE CHARACTERISTICS:
14     LENGTH: 51952 base pairs
15     TYPE: nucleic acid
16     STRANDEDNESS: single
17     TOPOLOGY: linear
18     MOLECULE TYPE: DNA (genomic)
19     US-08-947-823-1

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Query Match	5.5%;	Score 149.2;	DB 3;	Length 51952;
Best Local Similarity	49.5%;	Pred. No. 3e-32;		
Matches 512; Conservative	0;	Mismatches 498;	Indels 24;	Gaps 4

OY	4449	acataatggttgagcgtgatggtctcaagaagaacagttgttagaagaatctgcatlagaagct	508
Db	46729	ATTAATAATACCTTACGTTTGGGGGGAACAACAACCTTGATCTTGGAAAGCTCACCAAGG	467888
OY	509	actctgggnaaccacaagtcaccccgatgtgtcgggatggaggaataggtaaacacct	568
Db	46789	GATCGCGAGATCTCATGATCTTATTTGCATCAGTATGCGGGGTTCAGGTAAACACTCT	468488
OY	569	tagcaagaagatttacaatgatgatcaatctctatgtccgttttgatgtctatgtcctgg	628
Db	46849	TGGCTTACAAGATATACATGATGATGATGATTTAGCCGTTTGACCTTCGTGATGAT	469088
OY	629	ctaccatactcaacaagacaacaagaagaatttgcgtggccttcgcataccaaca	688
Db	46909	GCACGCTGACCAACGATGTGATGAGAAGATGTTGATATCAATTTTCACTCAAGTTA	469688
OY	689	tcaaaatgtagtagcagggttaagaatgatgtgtgaaacagagctagcagaacatgltacaga	748
Db	46969	GTGACTTCGAT-----TCAAAATTTGAGCTGACAAATTTGATGCTTCCTGTAATTAATTCGA	470282
OY	749	aaagtttaagaagaagaaggaacttaattgtcttgtagatatactcggagatgtlgaagtg	808
Db	47023	AACAACTGTTTGGAAAGAGATATTCTTATTTGTCTTGATGATGACTGTGGGATCTACTACAT	470882
OY	809	ggagatgctgtagagacgatgtcttccaactgaaacaatgacagagagctgaaatactgttga	868
Db	47083	GGGATGAGATTTAAACAAGACTTTTTC--CTGAAATCTAAGAAAGAGATGAGATTAATTTGA	471398
OY	869	ctaccggtaatgtagaagtagctgttctgtcgtggtgatagaatcttcttcttggyatga	928
Db	47140	CAACTCGGGAAAGGAATGGCTTTGCAATGGAACCTGAACCTGATCTCTTGAACCTTC	471998
OY	929	gcttcatgtagatcaagatgtagagttgtagtcttcttcaaaagtgcagcatcttccaagtgaag	988
Db	47200	GATTGCTTAAGACCAAGATGAAGTTGGGAACATATTAGCAAAAAGGCGCATTTGGGAATGAGA	472598
OY	989	cattaccataatgagttgtagagactgttctggaagaagcaatgcagatgaaatgtcaaggttaac	1048
Db	47260	GTTGCCCTGATGAATATTATAGATGTGCGGTAAAGAAATAGCCAAAATTTGTAAAGGGGCTTC	473198
OY	1049	caatacaactatgtcgtgtgtgcagaggtcttccaatctcaaaaggaagaatagatgtga	1108
Db	47320	CTTTGTGCGCTGATCTGATTTGCTGTGGAGTCATTTGCTGGAGGGGAAAAAGAAAGAGATGTGT	473798
OY	1109	aaactgtgtgctaaagatgtcaagatcatctgcgtcaacaatgatcatccgtatgaaagatgttcaac	1168
Db	47380	GCGTTGAAGTTCAAAGTATGTTGAGTCTTTTATTTTGAACAGTAAAGTGAAGTGAAGTATGA	474398

OY	1169	gtgtgcttggtgttggttaacgtaacgtacattgacaagagatctaaacaagctcttcgatt	1228
Db	47440	AAGTATATGAAATTAAGTTATGACCATTTACACATCACCTCAAGCATTGCTGTATP	47499
OY	1229	tcggaattcttcacgaagaacagtgatcttccagtgaaagatttgatgatacatgtag	1288
Db	47500	TTGCAGATTTTCCGANAAGCACACTTATTCACATCTATGATGATTGAATGTTTTCGGTG	47559
OY	1289	ctgaagggtctcct-----gaagcttgaaaatgatttgaagagaggttcgaagtgct	1342
Db	47560	CTGAAGCATTTTGTGGAAAGACAGGAGATGAAACAGTATGGAACAACAGTGGTGAAGATTATA	47619
OY	1343	tgcagaagctcttgcatagatgctctagtccttcgcgaagaagaagctcgagatgaaaca	1402
Db	47620	TGCAGATTTTAAATTACAGTACCTGGTAAATTTGTTCCATATGAGTATGAGTTATGCATGCA	47679
OY	1403	aaattagatcatgttaagttcatgattcctaataatgaacctgtgcgttgagagaagttcaaa	1462
Db	47680	A-----TTTCCAAATTCATGATCTTGTCATGACACTTTGTTGATTAAGAACACAGAA	47730
OY	1463	gggagaacatttt 1476	
Db	47731	AGGAAATTTGTTT 47744	

QY 1463 gggaacatttc 1476  
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Db 47731 AGGAAATTGTTT 47744

RESULT 13  
 US-08-947-823-4  
 Sequence 4, Application US/08947823  
 Patent No. 6114605  
 GENERAL INFORMATION:  
 APPLICANT: Williamson, Valerie M.  
 APPLICANT: Kaloshian, Isqouhl  
 APPLICANT: Yaghoobi, Jafar  
 APPLICANT: Bodeau, John  
 APPLICANT: Milligan, Stephen  
 TITLE OF INVENTION: Procedures and Materials for Confering  
 TITLE OF INVENTION: Pest Resistance in Plants  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Crew LLP  
 STREET: Two Embarcadero Center, Eighth Floor  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94111-3834  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/947,823  
 FILING DATE: 09-OCT-1997  
 CLASSIFICATION: 800  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US97/18802  
 FILING DATE: 09-OCT-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/028,191  
 FILING DATE: 10-OCT-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Bastian, Kevin L.  
 REGISTRATION NUMBER: 34,774  
 REFERENCE/DOCKET NUMBER: 023070-070210US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3982 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear

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? MOLECULE TYPE: CDNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 87..3860
? OTHER INFORMATION:
? OTHER INFORMATION:
? US-08-947-823-4
? /note= "Copy 2 CDNA for M1 nematode
? resistance gene of tomato"

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Query Match	5.4%;	Score 147.6;	DB 3;	Length 3982;
Best Local Similarity	49.4%;	Pred. No. 2.1e-32;		
Matches 511;	Conservative 0;	Mismatches 499;	Indels 24;	Gaps 4.

Oy	449	acatacgtttgcagcgtgacgtacacaaaggaacaacggtttgagaatcgtacgaacact	508
Db	1642	ATTAATAATTAATTGTAGGTTTGGAGSAGSAGACAACTTGATCTTGAAAGCACCACACTG	1701
Oy	509	actctbvggaaccacaagatccatccgatctgcggatbvggagatagtgaaacaacct	568
Db	1702	GACCCGCGAGATTAGATGCTATTTCATACACCGGTATGCCGGGTTCCAGGTAAACTTCT	1761
Oy	569	tagcaaaagagatttaacatgataatcattatgcgcgtttgatgtacatgcctcgtg	628
Db	1762	TGGCATTCAAAGTATACATGATTAAGTCACTTTCTTGACATTTTGACCTTGGTGCATGT	1821
Oy	629	ctaccatactcaacagcaacaacaaagaaatttgcttgcgtcttcgcatccaca	688
Db	1822	GCACGGTCGATCAAGATATGACGACACAGACTGTTCGATTCAAATTTTCAGTCAAGTTA	1881
Oy	669	tcaaaatgagatgacagtgtaaatgatgttggagaagacagctagcagacatgtaacga	748
Db	1882	GTGCGCTCAGAT----TCAAAATTTGAGTCAGAAATTTATGTGCTGTGAATTAATGCCGA	1935
Oy	749	aaagttaaagaagaagaaggtactaataatgtctctgagatgatactcgaagtbtgaagyt	808
Db	1936	AACAACGTGTTGGAAAGAGGTATCTTATGTCTTAGATGATGTGGGATCTACTACAT	1995
Oy	809	ggagatgagcgtgagacgagctgcttccaaatgaagacaatgcagggagtgaaatcgttga	868
Db	1996	TGGATGAGTTGACAAAGACCTTTTC--CTCAACCTTAAGAAAGAAAGATAGATTATTTTGA	2053
Oy	869	ctaccocgtaatgataagatgactgttatgctgtgttagagaaatttctctgcgaaatga	928
Db	2053	CAACTCGAGAAAGAGAGTGGCTTTCGATGGAAGAGTGAAACTGATCCTCTTGACCTTC	2112
Oy	929	gcttcacatgatacaagatgagatgttgagctcttccaagaatgcagcattttcaagtgaag	988
Db	2113	GATTGCTAAGACCCGATGAAGAAAGTTGGACATTTTAAATTAAGAAAGCACTTTGGTAATGGA	2173
Oy	989	cattaccataatgagcttcgagacgcttctggaaagaacaatgcagaatgataatgcacgggttac	1048
Db	2173	GTTGCCCTGATGAACCTATTGATGTGCGGTAAAGAAATTAACCCGAAATTTTAAAGGGCTTC	2233
Oy	1049	caactaactatgtcgttggtttgcagggcttccaaatctaagaagacatagaagaatgtga	1108
Db	2233	CTTTGGTGCGGATCTGATTGTGCTGGAGTCATTCTGGGAGGGAAGAAAGAAAGAGTGTGT	2293
Oy	1109	aaactgtgtctaaagaatgtaacatcgtctgcacaatgatcctgatbgaagaatgttcaac	1168
Db	2293	GCGTTGAGTTCAAAGATGTTAGATCTTTTATTTTGAACAGTGAAGGGAATGATGA	2353
Oy	1169	gtgtgctctgggtttgagttaacatcaactctgacaacgcgatatcaaaacatctcttcgcat	1228
Db	2353	AAGTTATATGATTAAGTTATAGACCATTTTACCAATCACTCAAGGCATGCTGTTCACT	2412
Oy	1229	tcggaattttccgaagaacagtatataatccagtgaagaatttgatbgaatcaatgatatg	1288
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Oy	1289	cttaggggggttctct-----gaagtggaaatgatatttgaaagagaggttggaaagtct	1342
Db	2473	CTGAAGGATTTGTGCAAAAGACGAGATGAAGGCTATACAAAGAAAGGGGAAAGATTTATA	2533

QY	1343	tgcaagagctgtcgtcgtatagttgtctcgtctcgtcaagagaagtcgaaatggaaca	1402
Db	2533	TGGATGATTTAAATTTCCAGAGCTTGATATTTGTTTCATAGTAGTAGTGATATCTGA	2552
QY	1403	aattagatcatctgaaggttcacgtacctaataatagctctgctgtagagaagttcaaa	1462
Db	2533	A-----TTTCCAAATTCATGATCTTGTCATGACATTTTGTTTGATATAAAGCAGAA	2643
QY	1463	ggagagaacattttt	1476
Db	2644	AGGAAATTTCTTT	2657

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	Query Match	Similarity	3.1%	Score	83.6	DB	3	Length	4465
	Best Local	Similarity	47.6%	Pred.	No. 5.7e-14				
	Matches	393	Conservative	0	Mismatches	409	Indels	24	Gaps
QY	518	aaccacaagatcccgcatgfcggaatgagggagcatagatgaacaacacttagcaaaag	577						
Db	781	ATCTGACAGTGGTTCCCTATTGTTGGAAATGGGCTGGCTGGCAGACAAACACTTGGTAAAG	840						
QY	578	aagttacaatgatgaatcaatcattcatgocgctttggaatgltcatgcctgggtacacatat	637						
Db	841	CCGTTATACATATATAGAGAGTGTGAAGAACCATTTTGCATTTTGAAAGCTTGCTTTTGCTTT	900						



